

GenCore version 5.1.6
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MM protein - protein search, using sw model

Run on: February 9, 2004, 09:56:08 ; Search time 18.2838 Seconds
(without alignments)
646.953 Million cell updates/sec

Title: US-09-981-876-200
Perfect score: 657
Sequence: 1 MACRCLSFLMGTFLSVSQT.....PVPQEDADYCVGVGFSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	430	65.4	123	2	S35302	B-cell protein 8HS
2	233.5	35.5	142	2	B28344	VpreB protein prec
3	229.5	34.9	142	2	A28344	VpreB protein prec
4	217.5	33.1	120	2	PS0055	Ig lambda chain pr
5	215.5	32.8	139	2	S00258	VpreB protein - hu
6	215.5	32.8	145	2	I57832	Vpre-B protein - h
7	213.5	32.5	232	2	S17399	Ig lambda chain pr
8	210.5	32.0	120	2	PS0056	Ig lambda chain pr
9	208.5	31.7	133	2	A28565	Ig lambda chain -
10	207.5	31.6	243	2	S25755	Ig lambda chain -
11	202	30.7	111	1	L6HUST	Ig lambda chain V-
12	200.5	30.5	118	2	A32529	Ig lambda chain pr
13	199	30.3	112	1	L6HUAR	Ig lambda chain V-
14	197	30.0	117	2	S04525	Ig lambda chain pr
15	196	29.8	136	2	S16848	Ig lambda chain V-
16	193.5	29.5	98	2	S36068	Ig lambda chain -
17	191.5	29.1	99	2	S36058	Ig lambda chain -
18	191.5	29.1	132	2	A55410	Ig light chain V r
19	191	29.1	235	2	S25758	Ig lambda chain -
20	190.5	29.0	216	2	S69130	Ig lambda chain (D
21	189.5	28.8	234	2	A39956	Ig lambda chain pr
22	186.5	28.4	99	2	S36057	Ig lambda chain -
23	186.5	28.4	111	1	L2HUMC	Ig lambda chain V-
24	185	28.2	111	1	L6HULT	Ig lambda chain pr
25	185	28.2	131	1	L6HUEB	Ig lambda chain pr
26	184.5	28.1	111	1	L2HUBO	Ig lambda chain V-
27	184.5	28.1	233	2	S25744	Ig lambda chain -
28	183.5	27.9	130	1	L1HUBL	Ig lambda chain pr
29	182.5	27.8	99	2	S36051	Ig lambda chain -

30 182.5 27.8 99 2 S36053 Ig lambda chain -
31 182.5 27.8 117 2 S23627 Ig lambda chain pr
32 182.5 27.8 233 2 S25752 Ig lambda chain -
33 182.5 27.8 235 2 S25750 Ig lambda chain -
34 181.5 27.6 111 2 S46397 Ig lambda chain V
35 181.5 27.6 112 2 S31515 Ig lambda chain pr
36 181.5 27.6 117 2 S04526 Ig lambda chain pr
37 181.5 27.6 118 2 S12627 Ig lambda chain -
38 181.5 27.6 234 2 S25757 Ig lambda chain V
39 180.5 27.5 107 2 B45516 Ig lambda chain V-
40 180.5 27.5 111 1 L1HUNG Ig lambda chain pr
41 180.5 27.5 112 1 L2HUNG Ig lambda chain pr
42 180.5 27.5 117 1 LVHU2 Ig lambda chain pr
43 180.5 27.5 132 2 PL0114 Ig lambda chain pr
44 180.5 27.5 132 2 S04937 Ig lambda chain pr
45 180 27.4 108 2 S38498 Ig lambda chain -

ALIGNMENTS

RESULT 1
S35302
B-cell protein 8HS-20 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C/Accession: S35302
R/Shirasawa, T.; Ohnishi, K.; Hagiwara, S.; Shigenoto, K.; Takebe, Y.; Rajewsky, K.; Te
EMBO J. 12, 1827-1834, 1993
A/Title: A novel gene product associated with mu chains in immature B cells.
A/Reference number: S35302; MUID:93259124; PMID:8491176
A/Accession: S35302
A/Molecule type: DNA
A/Residues: 1-123 <SHI>
A/Cross-references: EMBL:DI3208; NID:g286064; PIDN:BAA02495.1; PID:g286065
C/Genetics:
A/Gene: 8HS-20
A/Introns: 18/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: B-cell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-123/Product: B-cell protein 8HS-20 #status predicted <MAT>
Query Match 65.4%; Score 430; DB 2; Length 123;
Best Local Similarity 66.1%; Pred. No. 2.9e-36;
Matches 82; Conservative 14; Mismatches 26; Indels 2; Gaps 2;
QY 1 MACRCLSFLMGTFLSVSQTVAQLDALLVFFQVLAQLSCTLSPOKVTIRDYGVSWYQQ 59
Db 1 MACRCLEPLLLIGTFVAVFQPTLPDPAFVSFFQDAHLSCITNSCHATAGDIGVSWYQQ 60
QY 60 RAGSAPRVLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYCVSVGY 119
Db 61 QPGSAP-HLLYYABEEHYRPADIPDRFSATVDAAHNACILITISVLPEDDADYFCSIAH 119
QY 120 GFSP 123
Db 120 rFEP 123
RESULT 2
B28344
VpreB protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 05-Nov-1999
C/Accession: B28344
R/Kudo, A.; Melchers, F.
EMBO J. 6, 2267-2272, 1987
A/Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be s
A/Reference number: A91077; MUID:88029315; PMID:3117530
A/Accession: B28344
A/Molecule type: DNA
A/Residues: 1-142 <KUD>

A;Cross-references: GB:X05563; GB:Y00079; NID:G55415; PIDN:CAA29077.1; PID:G55416
A;Note: the authors translated the codon GAG for residue 110 as Gln
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F:20-142/Product: VpreB protein #status predicted <Mar>

Query Match 35.5%; Score 233.5; DB 2; Length 142;

Best Local Similarity 54.7%; Pred. No. 2.2e-16;
Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

QY 33 GQVQLSCTLSQPVHTRDYGVSQYQVQAGSAPRYLLYRSSEDRHRPADIPDRFSAKD 92
DB 34 GATIRLSCTLSNDH-NIGIYSIYVYQKPGHPFRFLRYFSHSDKHQGPDIIPRSGSKD 92

QY 93 EAHNACVLTISPVEDDADYCSVG 118

DB 93 TARNLGYLSISELQPEDEAVYICAVG 118

RESULT 3

A28344

VpreB protein precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000

C;Accession: A28344

R;Kudo, A.; Melchers, F.

EMBO J. 6, 2267-2272, 1987

A;Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se
A;Reference number: A31077; MUID:88029315; PID:3117330

A;Accession: A28344

A;Molecule type: DNA

A;Residues: 1-142 <KUD>

A;Cross-references: GB:X05556; GB:Y00079; NID:G55409; PIDN:CAA29077.1; PID:G55410

A;Note: the authors translated the codon GAG for residue 110 as Gln

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F:20-142/Product: VpreB1 protein #status predicted <MAT>

Query Match

Best Local Similarity 34.9%; Score 229.5; DB 2; Length 142;

Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;

QY 33 GQVQLSCTLSQPVHTRDYGVSQYQVQAGSAPRYLLYRSSEDRHRPADIPDRFSAKD 92

DB 34 GATIRLSCTLSNDH-NIGIYSIYVYQKPGHPFRFLRYFSHSDKHQGPDIIPRSGSKD 92

QY 93 EAHNACVLTISPVEDDADYCSVG 118

DB 93 TTRNLGYLSISELQPEDEAVYICAVG 118

RESULT 4

PS0055

IG lambda chain precursor V-II region - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999

C;Accession: PS0055

R;Hayzer, D.J.; Jaton, J.C.

Gene 80, 185-191, 1989

A;Title: Cloning and sequencing of two functional rabbit germ-line immunoglobulin V lamb

A;Reference number: A31614; MUID:9006781; PMID:2507399

A;Accession: PS0055

A;Molecule type: DNA

A;Residues: 1-120 <HAY>

A;Cross-references: GB:M07840; NID:G341760; PIDN:AAA31363.1; PID:G552407

A;Note: the authors translated the codon TTG for residue 97 as Trp

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-120/Product: Ig lambda chain V-II region #status predicted <MAT>

Query Match

Best Local Similarity 33.1%; Score 217.5; DB 2; Length 120;

Matches 41.2%; Pred. No. 7.5e-15;

Matches 49; Conservative 17; Mismatches 44; Indels 9; Gaps 3;
QY 5 CLSLFMCTFL----SVSTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
DB 3 CYPLELLTLTLCQTSUSQPVLTQSPSVSAALGASAKLTCTLSSAHT---YTIWYQQQ 59
QY 61 AGSAPRYLLYRSSEDRHRPADIPDRFSAAKDBAHNACVLTISPVEDDADYCSVG 119
DB 60 QGEAPRYLMQLKSGSYTKGTGVDFRFGSSGADR--YLLIPSVQADDEADYVCADY 116

RESULT 5

S00258

VpreB protein - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Nov-1999

C;Accession: S00258

R;Bauer, S.R.; Kudo, A.; Melchers, F.

EMBO J. 7, 111-116, 1988

A;Title: Structure and pre-B lymphocyte restricted expression of the VpreB gene in hum

A;Reference number: S00258; MUID:88196069; PMID:3258819

A;Accession: S00258

A;Molecule type: DNA

A;Residues: 1-139 <BAU>

A;Cross-references: EMBL:M34927; NID:G340304; PIDN:AAA61292.1; PID:G340305

C;Genetics:

A;Gene: GDB:VPREB1

A;Cross-references: GDB:120493; OMIM:146770

A;Map position: 22q11.2-22q11.2

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match

Best Local Similarity 32.8%; Score 215.5; DB 2; Length 139;

Matches 47; Conservative 13; Mismatches 39; Indels 1; Gaps 1;

QY 19 QTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSSEDRH 78

DB 20 QPVLLQPPAMSSALGTTRITLCTLRNDH-DIGVSYVYQORCHPFRFLRYFSQSDKS 78

QY 79 RPADIPDRFSAAKDBAHNACVLTISPVEDDADYCSVG 118

DB 79 QGPVQPPFRFGSKDVARNRGYLSISELQPEDEAMYYICAMG 118

RESULT 6

I57832

VPre-B protein - human

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I57832

R;Guelpa-Ponlupt, V.; Bossy, D.; Alzati, P.; Fumoux, P.; Fougereau, M.; Schiff, C.

Mol. Immunol. 31, 1099-1108, 1994

A;Title: The human pre-B cell receptor: structural constraints for a tentative model of

A;Reference number: I57832; MUID:95021318; PMID:7935499

A;Accession: I57832

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-145 <RES>

A;Cross-references: GB:S74019; NID:G693810; PIDN:AA32118.1; PID:G693811

C;Genetics:

A;Gene: Vpre-B

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match

Best Local Similarity 32.8%; Score 215.5; DB 2; Length 145;

Matches 47; Conservative 13; Mismatches 39; Indels 1; Gaps 1;

QY 19 QTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSSEDRH 78

DB 20 QPVLLQPPAMSSALGTTRITLCTLRNDH-DIGVSYVYQORCHPFRFLRYFSQSDKS 78

Biochem. J. 195, 561-572, 1981
A:Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light chain (c)
A:Reference number: A01987; MUID:82091000; PMID:6797401
A:Contents: amyloid protein AR
A:Accession: A01987
A:Molecule type: protein
A:Residues: 1-112 <SLZ>
A:Note: about half of the lambda chain C region is missing from this protein
A:Comment: This protein was isolated from the spleen of a patient with amyloidosis.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a trimeric complex.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>
F:22-91/Disulfide bonds: #status predicted

Query Match 30.3%; Score 199; DB 1; Length 112;
Best Local Similarity 44.2%; Pred. No. 5.1e-13;
Matches 42; Conservative 18; Mismatches 29; Indels 6; Gaps 2;

QY 21 VLAQDALLVFPQVQAQLSCTLSQPHVTIRDYGVSVYQQRAGSAPRYLYRSEEDHRRP 80
Db 3 MLTQPHSVSESPGKTVTFCTSGG--SIADSFVQVYQQRPGSAPTIVY---DDNQRP 56
QY 81 ADIPRFAAKDEAHNAACVLTISPQVEDDADYYC 115
Db 57 SGVPRFSGSIDSSANSASLTISGLKTEDEADYYC 91

RESULT 14
S04525
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04525
R:Alexandre, D.; Chuchana, P.; Brockly, F.; Blancher, A.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 17, 3975, 1989
A:Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup 1
A:Reference number: S04525; MUID:89282401; PMID:2499871
A:Accession: S04525
A:Molecule type: DNA
A:Residues: 1-117 <ALE>
A:Cross-references: EMBL:X14615; NID:933397; PIDN:CAA32769.1; PID:g736246
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 30.0%; Score 197; DB 2; Length 117;
Best Local Similarity 40.3%; Pred. No. 8.6e-13;
Matches 50; Conservative 23; Mismatches 41; Indels 10; Gaps 5;

QY 1 MACR-CLSFLLMTGTFUSQTVLAQLDALLVFPQVQAQLSCTLSQPHVTIRDYGVSVYQ 59
Db 1 MTCSPILLTLTHCTGSAQSVLTQPPSVAPGQKVTISCGSS--DMGNVAVSWYQQ 58
QY 60 RAGSAPRYLYRSEEDHRRPADIPRFAAKDEAHNAACVLTISPQVEDDADYYC 119
Db 59 LPGTAPKLLIY----ENNKRPSPGIDPRFSGSK--SGTSATLGLTGLWPEDEADYYC-LAW 111
QY 120 GFSP 123
Db 112 DTSP 115

RESULT 15
S16848
Ig lambda chain V-II region precursor - human

A:Reference number: A01988
A:Accession: A01988
A:Molecule type: protein
A:Residues: 1-111 <SOL>
A:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a trimeric complex.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>
F:22-91/Disulfide bonds: #status predicted

Query Match 30.7%; Score 202; DB 1; Length 111;
Best Local Similarity 45.3%; Pred. No. 2.5e-13;
Matches 43; Conservative 15; Mismatches 31; Indels 5; Gaps 2;

QY 21 VLAQDALLVFPQVQAQLSCTLSQPHVTIRDYGVSVYQQRAGSAPRYLYRSEEDHRRP 80
Db 3 MLTQPHSVSESPGKTVTFCTSGG--TIAGYVQVYQQRPGSAPTIVF---EDTQRP 56
QY 81 ADIPRFAAKDEAHNAACVLTISPQVEDDADYYC 115
Db 57 SGVPRFSGSIDSSANSASLTISGLKTEDEADYYC 91

RESULT 12
A32529
Ig lambda chain precursor V region (clone pD8) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Jun-1990 #sequence_revision 23-Nov-1991 #text_change 16-Aug-1996
C:Accession: A32529
R:Hayzer, D.J.; Duvoisin, R.M.; Jaton, J.C.
Biochem. J. 245, 691-697, 1987
A:Title: cDNA clones encoding rabbit immunoglobulin lambda chains. Evidence for length variation in the variable region
A:Reference number: A90338; MUID:88024122; PMID:3117050
A:Accession: A32529
A:Molecule type: mRNA
A:Residues: 1-118 <HAY>
A:Cross-references: GB:M25617
A:Note: the authors translated the codon TTG for residue 37 as Phe
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.5%; Score 200.5; DB 2; Length 118;
Best Local Similarity 42.3%; Pred. No. 3.8e-13;
Matches 44; Conservative 14; Mismatches 41; Indels 5; Gaps 2;

QY 16 SVSQTVLAQLDALLVFPQVQAQLSCTLSQPHVTIRDYGVSVYQQRAGSAPRYLYRSE 75
Db 3 SLSPQVLTQPSAAALGASAKLTCTLSAKTSL---VEVYQHQGEAPRYLMWLKDG 59
QY 76 DHRPADIPRFAAKDEAHNAACVLTISPQVEDDADYYC 119
Db 60 SYTKGTGVDRFSGSSGGADR--YLIISVQADDEADYYC 101

RESULT 13
L6HUAR
Ig lambda chain V-VI region (AR) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Mar-2000
C:Accession: A01987

Biochem. J. 195, 561-572, 1981
A:Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light chain (c)
A:Reference number: A01987; MUID:82091000; PMID:6797401
A:Contents: amyloid protein AR
A:Accession: A01987
A:Molecule type: protein
A:Residues: 1-112 <SLZ>
A:Note: about half of the lambda chain C region is missing from this protein
A:Comment: This protein was isolated from the spleen of a patient with amyloidosis.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a trimeric complex.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>
F:22-91/Disulfide bonds: #status predicted

Query Match 30.3%; Score 199; DB 1; Length 112;
Best Local Similarity 44.2%; Pred. No. 5.1e-13;
Matches 42; Conservative 18; Mismatches 29; Indels 6; Gaps 2;

QY 21 VLAQDALLVFPQVQAQLSCTLSQPHVTIRDYGVSVYQQRAGSAPRYLYRSEEDHRRP 80
Db 3 MLTQPHSVSESPGKTVTFCTSGG--SIADSFVQVYQQRPGSAPTIVY---DNQRP 56
QY 81 ADIPRFAAKDEAHNAACVLTISPQVEDDADYYC 115
Db 57 SGVPRFSGSIDSSANSASLTISGLKTEDEADYYC 91

RESULT 14
S04525
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04525
R:Alexandre, D.; Chuchana, P.; Brockly, F.; Blancher, A.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 17, 3975, 1989
A:Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup 1
A:Reference number: S04525; MUID:89282401; PMID:2499871
A:Accession: S04525
A:Molecule type: DNA
A:Residues: 1-117 <ALE>
A:Cross-references: EMBL:X14615; NID:933397; PIDN:CAA32769.1; PID:g736246
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 30.0%; Score 197; DB 2; Length 117;
Best Local Similarity 40.3%; Pred. No. 8.6e-13;
Matches 50; Conservative 23; Mismatches 41; Indels 10; Gaps 5;

QY 1 MACR-CLSFLLMTGTFUSQTVLAQLDALLVFPQVQAQLSCTLSQPHVTIRDYGVSVYQ 59
Db 1 MTCSPLLLTLLHCTCSWAQSVLTQPPSVAPGQKVTISCGSS--DMGNVAVSWYQ 58
QY 60 RAGSAPRYLYRSEEDHRRPADIPRFAAKDEAHNAACVLTISPQVEDDADYYCVGY 119
Db 59 LPGTAPKLLIY----ENNKRPSPGIDPRFSGSK--SGTSATLGLTGLWPEDEADYYC-LAW 111
QY 120 GFSP 123
Db 112 DTSP 115

RESULT 15
S16848
Ig lambda chain V-II region precursor - human

A:Reference number: A01988
A:Accession: A01988
A:Molecule type: protein
A:Residues: 1-111 <SOL>
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a trimeric complex.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>
F:22-91/Disulfide bonds: #status predicted

Query Match 30.7%; Score 202; DB 1; Length 111;
Best Local Similarity 45.3%; Pred. No. 2.5e-13;
Matches 43; Conservative 15; Mismatches 31; Indels 5; Gaps 2;

QY 21 VLAQDALLVFPQVQAQLSCTLSQPHVTIRDYGVSVYQQRAGSAPRYLYRSEEDHRRP 80
Db 3 MLTQPHSVSESPGKTVTFCTSGG--TIAGYVQVYQQRPGSAPTIVF---EDTQRP 56
QY 81 ADIPRFAAKDEAHNAACVLTISPQVEDDADYYC 115
Db 57 SGVPRFSGSIDSSANSASLTISGLKTEDEADYYC 91

RESULT 12
A32529
Ig lambda chain precursor V region (clone pD8) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Jun-1990 #sequence_revision 23-Nov-1991 #text_change 16-Aug-1996
C:Accession: A32529
R:Hayzer, D.J.; Duvoisin, R.M.; Jaton, J.C.
Biochem. J. 245, 691-697, 1987
A:Title: cDNA clones encoding rabbit immunoglobulin lambda chains. Evidence for length variation in the variable region
A:Reference number: A90338; MUID:88024122; PMID:3117050
A:Accession: A32529
A:Molecule type: mRNA
A:Residues: 1-118 <HAY>
A:Cross-references: GB:M25617
A:Note: the authors translated the codon TTG for residue 37 as Phe
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.5%; Score 200.5; DB 2; Length 118;
Best Local Similarity 42.3%; Pred. No. 3.8e-13;
Matches 44; Conservative 14; Mismatches 41; Indels 5; Gaps 2;

QY 16 SVSQTVLAQLDALLVFPQVQAQLSCTLSQPHVTIRDYGVSVYQQRAGSAPRYLYRSE 75
Db 3 SLSPQVLTQPSAAAALGASAKLTCTLSAKTSL---VEVYQHQGEAPRYLMWLKDG 59
QY 76 DHRPADIPRFAAKDEAHNAACVLTISPQVEDDADYYCVGY 119
Db 60 SYTKGTGVDRFSGSSGGADR--YLIISVQADDEADYYCGVDY 101

RESULT 13
L6HUAR
Ig lambda chain V-VI region (AR) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Mar-2000
C:Accession: A01987

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

un on: February 9, 2004, 12:31:07 ; Search time 11.6351 Seconds
(without alignments)
497.139 Million cell updates/sec

File: US-09-981-876-200

Effect score: 657

Sequence: 1 MACRCLSLFLMGTFILSVSQT.....PVQPEDDADYCVSVGYGFSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	657	100.0	123	1 VPR3_HUMAN	Q9uk13 homo sapien
2	233.5	35.5	142	1 VPR2_MOUSE	P13373 mus musculu
3	229.5	34.9	142	1 VPR1_MOUSE	P13372 mus musculu
4	215.5	32.8	145	1 VPRE_HUMAN	P12018 homo sapien
5	202	30.7	111	1 LV6C_HUMAN	P06317 homo sapien
6	199	30.3	112	1 LV6A_HUMAN	P01721 homo sapien
7	186.5	28.4	111	1 LV2F_HUMAN	P01709 homo sapien
8	185.5	28.2	111	1 LV2L_HUMAN	P80422 homo sapien
9	185	28.2	111	1 LV6D_HUMAN	P06318 homo sapien
10	184.5	28.1	111	1 LV6E_HUMAN	P06319 homo sapien
11	184.5	28.1	111	1 LV2G_HUMAN	P01710 homo sapien
12	183.5	27.9	130	1 LV1D_HUMAN	P06316 homo sapien
13	180.5	27.5	111	1 LV1G_HUMAN	P01702 homo sapien
14	180.5	27.5	112	1 LV2K_HUMAN	P04209 homo sapien
15	180.5	27.5	117	1 LV0A_HUMAN	P04211 homo sapien
16	179	27.2	111	1 LV2I_HUMAN	P01712 homo sapien
17	177.5	27.0	109	1 LV2J_HUMAN	P01708 homo sapien
18	175	26.6	108	1 LV3A_HUMAN	P01714 homo sapien
19	175	26.6	108	1 LV5A_HUMAN	P01719 homo sapien
20	173	26.3	109	1 LV1F_HUMAN	P04208 homo sapien
21	173	26.3	111	1 LV3B_HUMAN	P80748 homo sapien
22	172.5	26.3	110	1 LV2J_HUMAN	P01713 homo sapien
23	168.5	25.6	111	1 LV2B_HUMAN	P01705 homo sapien
24	167	25.4	106	1 LV4D_HUMAN	P01718 homo sapien
25	166	25.3	106	1 LV4B_HUMAN	P01716 homo sapien
26	166	25.3	111	1 LV1C_HUMAN	P01717 homo sapien
27	165	25.1	107	1 LV4C_HUMAN	P01700 homo sapien
28	164.5	25.0	112	1 LV1B_HUMAN	P01711 homo sapien
29	163.5	24.9	111	1 LV2H_HUMAN	P06887 homo sapien
30	163.5	24.9	112	1 LV1H_HUMAN	P01715 homo sapien
31	163	24.8	106	1 LV4A_HUMAN	P01622 homo sapien
32	162.5	24.7	109	1 RV3D_HUMAN	P01704 homo sapien
33	162.5	24.7	111	1 LV2A_HUMAN	P01704 homo sapien

34	162	24.7	109	1 LV1I_HUMAN	P06888 homo sapien
35	161.5	24.6	129	1 KV3L_HUMAN	P18135 homo sapien
36	160.5	24.4	108	1 KV3A_HUMAN	P01619 homo sapien
37	159.5	24.3	111	1 LV2C_HUMAN	P01706 homo sapien
38	158.5	24.1	111	1 LV2D_HUMAN	P01707 homo sapien
39	158	24.0	113	1 LVI_CHICK	P04210 gallus gall
40	157.5	24.0	109	1 KV3E_HUMAN	P01620 homo sapien
41	157.5	24.0	109	1 KV3G_HUMAN	P04206 homo sapien
42	155.5	23.7	129	1 KV3M_HUMAN	P18136 homo sapien
43	153	23.3	112	1 LV6B_HUMAN	P01722 homo sapien
44	151.5	23.1	115	1 KV3I_HUMAN	P04433 homo sapien
45	151	23.0	106	1 LV4E_HUMAN	P06889 homo sapien

ALIGNMENTS

RESULT 1
VPR3_HUMAN STANDARD; PRT; 123 AA.
AC Q9UK13;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pre-B lymphocyte protein 3 precursor (VpreB3 protein) (N27C7-2).
GN VPREB3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP RP
RF MEDLINE=20169186; PubMed=10702669;
RA Roenert O., Mattei M.-G., Delattre O., Schiff C.;
RT "VPREB3: cDNA characterization and expression in human and chromosome
mapping in human and mouse.";
RL Cytogenet. Cell Genet. 87:205-208(1999).
RN [2]
RP RP
RF SEQUENCE FROM N.A.
RA Shimizu N., Minosima S., Kawasaki K., Sasaki T., Hosono K.;
RT "Molecular cloning of N27C7-2 gene.";
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP RP
RF SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshilyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:15899-15903(2002).
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN B CELL PRECURSORS. EXPRESSED IN
FETAL LIVER, BONE MARROW, SPLEEN, AND LYMPH NODE.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC EMBL; AF163825; AAF09451.1; -
 CC EMBL; AB050772; BAB83034.1; -
 CC EMBL; BC020666; AAH20666.1; -
 CC HSSP; P01709; 2MCG
 CC Genew; HGNC.12710; VPREB3.
 CC MIM; 605017.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PSS0835; IG LIKE; 1.
 CC Immunoglobulin domain; B-cell; Signal.
 CC SIGNAL 1 20 POTENTIAL.
 CC CHAIN 21 123 PRE-B LYMPHOCYTE PROTEIN 3.
 CC DOMAIN 21 123 IG-LIKE.
 CC DISULFID 40 115 BY SIMILARITY.
 CC SEQUENCE 123 AA; 13710 MW; BF09AC5196059E85 CRC64;

Query Match 100.0%; Score 657; DB 1; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-62;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MACRCLSFLMGFTLSVQSVTLAQDLALVPPGVAQLSCTLSQPHVTIRDYGVSWYQQR 60
 DB 1 MACRCLSFLMGFTLSVQSVTLAQDLALVPPGVAQLSCTLSQPHVTIRDYGVSWYQQR 60
 QY 61 AGSAPRYLLYRSEEDHRRPADIPRFAAKDEAHNACVLIISVPQEDDADYCVSGYG 120
 DB 61 AGSAPRYLLYRSEEDHRRPADIPRFSNAKDEAHNACVLIISVPQEDDADYCVSGYG 120
 QY 121 FSP 123
 DB 121 FSP 123

RESULT 2
 ID VP2 MOUSE STANDARD; PRT; 142 AA.
 AC P13373;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Immunoglobulin omega chain precursor (VpreB2 protein).
 GN VPREB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X DBA/2J;
 RX MEDLINE=88029315; PubMed=3117530;
 RA Kudo A., Melchers F.;
 RT "A second gene, VpreB in the lambda 5 locus of the mouse, which
 RT appears to be selectively expressed in pre-B lymphocytes.";
 RL EMO J. 6:2267-2272(1987).
 CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
 CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
 CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
 CC STEPS OF B-CELL DIFFERENTIATION.
 CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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CC EMBL; X05563; CAA90077.1; -
 CC PIR; B28344; B28344.
 CC HSSP; P01607; IREI.
 CC MGD; MGI.98937; Vpreb2.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PSS0835; IG LIKE; 1.
 CC Immunoglobulin domain; B-cell; Signal.
 CC SIGNAL 1 19 POTENTIAL.
 CC CHAIN 20 142 IMMUNOGLOBULIN OMEGA CHAIN.
 CC DOMAIN 20 41 FRAMEWORK-1.
 CC DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.
 CC DOMAIN 57 70 FRAMEWORK-2.
 CC DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.
 CC DOMAIN 82 115 FRAMEWORK-3.
 CC DISULFID 41 115 BY SIMILARITY.
 CC SEQUENCE 142 AA; 16052 MW; 7EA7128A4E63D920 CRC64;

Query Match 35.5%; Score 233.5; DB 1; Length 142;
 Best Local Similarity 54.7%; Pred. No. 1, 1e-17;
 Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;
 QY 33 GOVAQLSCTLSQPHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIPRFSNAKD 92
 DB 34 GATRLSCTLSNDH-NIGYISYVYQQRPGHPRLLYFHSKQGPDIIPRFSKGD 92
 QY 93 EAHNACVLIISVPQEDDADYCVSG 118
 DB 93 TARNGLVLSISELQPEDEAVYICAVG 118

RESULT 3
 ID VP1 MOUSE STANDARD; PRT; 142 AA.
 AC P13372;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Immunoglobulin iota chain precursor (VpreB1 protein).
 GN VPREB1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X DBA/2J;
 RX MEDLINE=88029315; PubMed=3117530;
 RA Kudo A., Melchers F.;
 RT "A second gene, VpreB in the lambda 5 locus of the mouse, which
 RT appears to be selectively expressed in pre-B lymphocytes.";
 RL EMO J. 6:2267-2272(1987).
 CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
 CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
 CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
 CC STEPS OF B-CELL DIFFERENTIATION.
 CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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```

R R EMBL; X05556; CAA29071.1; -.
R R EMBL; X05557; CAA29072.1; -.
R R PIR; A28344; A28344.
R R HSP; P01607; IREI.
R R MGD; MG1:98936; VpreB1.
R R GO; GO:0005886; C:plasma membrane; IPI.
R R GO; GO:0004872; P:receptor activity; IPI.
R R GO; GO:000097; P:phenopolesis; IMP.
R R GO; GO:0006955; P:immune response; IPI.
R R InterPro; IPR007110; IG-like.
R R InterPro; IPR003006; IG_MHC.
R R InterPro; IPR003596; IG_V.
R R Pfam; PF00047; ig; 1.
R R SMART; SM00406; IGV; 1.
R R PROSITE; PS0835; IG_LIKE; 1.
R R Immunoglobulin domain; B-cell; Signal.
T T SIGNAL 1 19 POTENTIAL.
T T CHAIN 20 142 IMMUNOGLOBULIN IOTA CHAIN.
T T DOMAIN 20 41 FRAMEWORK-1.
T T DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.
T T DOMAIN 57 70 FRAMEWORK-2.
T T DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.
T T DOMAIN 82 115 FRAMEWORK-3.
T T DISULFID 41 115 BY SIMILARITY.
T T SEQUENCE 142 AA; 16125 MW; 2E18BF963A0F48C CRC64;

Query Match 34.9%; Score 229.5; DB 1; Length 142;
Best Local Similarity 53.5%; Pred. No. 2.9e-17;
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;

33 QQVAQLSCLSPQHTIRDYGVSVYQQRAGSAPRYLLYYSRESDHRPADIPDRSAKD 92
34 GATIRLSCLTNDH-NIGIYIYVQQRGPHPRFLRYFSHSDKHQGEDIPRFSGSKD 92

93 EAHNACVLTSVPQEDDADYCVSG 118
93 TRRNGLYSLSLEQDEAVYCVAG 118

RESULT 4
VPRE_HUMAN STANDARD; PRT; 145 AA.
AC P12018;
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Immunoglobulin iota chain precursor (V(pre)B protein) (VpreB protein)
DE (CD179a antigen).
DE VPREB1 OR VPREB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=9502118; PubMed=7935499;
RA Guelpa-Fonlupt V., Bossy D., Alzari P., Fumoux F., Fougereau M.,
RA Schiff C.;
RT "The human pre-B cell receptor: structural constraints for a tentative
RT model of the pseudo-light (psi L) chain.";
RL Mol. Immunol. 31:1099-1108(1994).
[2]_
RP SEQUENCE FROM N.A.
RX MEDLINE=97228902; PubMed=9074928;
RA Kawaaki K., Minoshima S., Mine E., Shibuya K., Shintani A.,
RA Schmeits J.L., Wang J., Shimizu N.;
RT "One-megabase sequence analysis of the human immunoglobulin lambda
RT gene locus.";
RL Genome Res. 7:250-261(1997).

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[3]
RN RP SEQUENCE OF 1-139 FROM N.A.
RX MEDLINE=88196069; PubMed=3258819;
RA Bauer S.R., Kudo A., Melchers F.;
RT "Structure and pre-B lymphocyte restricted expression of the VpreB in
RT humans and conservation of its structure in other mammalian
RT species.";
RL EMBL J. 7:111-116(1988).
CC -1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC STEPS OF B-CELL DIFFERENTIATION.
CC -1- SUBUNIT: Associates non-covalently with IGLL1.
CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- DATABASE: NAME=PROV; NOTE=PROV 1:59-63(2000);
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/574153212_g.htm".
CC -----
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EMBL; D86992; BAAL9987.1; -.
EMBL; D88270; BAA20030.1; -.
EMBL; S74019; AAB32118.1; -.
EMBL; M34927; AAA61292.1; -.
PIR; I57832; I57832.
PIR; S00258; S00258.
HSP; P80748; 2LOI.
Gene; HGNC:12709; VPREB1.
MIM; 605141; -.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
Immunoglobulin domain; B-cell; Signal; Antigen.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 145 IMMUNOGLOBULIN IOTA CHAIN.
FT DOMAIN 20 41 FRAMEWORK-1.
FT DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 70 FRAMEWORK-2.
FT DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 115 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT CONFLICT 10 10 L -> H (IN REF. 3).
SQ SEQUENCE 145 AA; 16605 MW; 197665B13AF64D46 CRC64;

Query Match 32.8%; Score 215.5; DB 1; Length 145;
Best Local Similarity 47.0%; Pred. No. 9e-16;
Matches 47; Conservative 13; Mismatches 39; Indels 1; Gaps 1;

QY 19 QTVLAQLDALLVFGCVQVLAQLSCLSPQHTIRDYGVSVYQQRAGSAPRYLLYYSRESDHH 78
Db 20 QPVLLHQPPAMSSALGTTIRLTCTLNDH-DIGVSVYVYQQRGPHPRFLRYFSQSDKS 78
QY 79 RPADIPIRPSAAKRAHNAVCVLT-SPVQPEDADYCVSG 118
Db 79 QGPQVPRFSGSKDVARNRGVLSISLEQDEAVYCVAG 118

RESULT 5
ID LV6C_HUMAN STANDARD; PRT; 111 AA.
AC P06317;


```

DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-VI region SUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Solomon A., Kyle R.A., Frangione B.;
RT "Light chain variable region subgroups of monoclonal immunoglobulins
in amyloidosis AL";
RL (in) Glenner G.G., Cessman E.P., Benditt E.P., Calkins E.,
Cohen A.S., Zucker-Franklin D. (eds.); New York (1986).
RL Amyloidosis, pp.449-462, Plenum Press, New York (1986).
DR PDB; 1CD0; 06-MAR-00.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 22
FT DOMAIN 23 35
FT DOMAIN 36 50
FT DOMAIN 51 57
FT DOMAIN 58 91
FT DOMAIN 92 100
FT DOMAIN 101 111
FT DISULFID 22 91
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12247 MW; 0941DD547D983598 CRC64;

Query Match 30.7%; Score 202; DB 1; Length 111;
Best Local Similarity 45.3%; Pred. No. 1.8e-14;
Matches 43; Conservative 15; Mismatches 31; Indels 6; Gaps 2;

QY 21 VLAQLDALLVFPQVQAQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYYRSEDHHRP 80
Db 3 MLTQPHSVESFGKTVISCTSDG--FIAGYVQVQYQRPGRAPTTVIF----EDTQRP 56

QY 81 ADIPDRFSAKDEAHNACVLTISVPQPEDDADYIC 115
Db 57 SGVPDRFSGSIDRSSNSASLTISGLQTEDEADYIC 91

RESULT 6
LV6A HUMAN STANDARD; PRT; 112 AA.
AC P01721;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-VI region AR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (AMYLID PROTEIN AR).
RX MEDLINE=92091000; PubMed=6797401;
RA Sletten K., Natvig J.B., Husby G., Juul J.;
RT "The complete amino acid sequence of a prototype
immunoglobulin-lambda light-chain-type amyloid-fibril protein AR";
RL Biochem. J. 195:561-572(1981).
CC -1- MISCELLANEOUS: ABOUT HALF OF THE LAMBDA CHAIN C REGION IS MISSING
FROM THIS PROTEIN.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A
PATIENT WITH AMYLOIDOSIS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A01987; LGHUA8.
DR HSP; P01709; 2MCG.
DR GO; GO:0005576; C-extracellular; NAS.
DR GO; GO:0003823; P-antigen binding activity; NAS.
DR GO; GO:0006955; P-immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 107
FT NON TER 112 112
SQ SEQUENCE 112 AA; 11918 MW; 570BCD9A368EF1FE CRC64;

Query Match 30.3%; Score 199; DB 1; Length 112;
Best Local Similarity 44.2%; Pred. No. 3.7e-14;
Matches 42; Conservative 18; Mismatches 29; Indels 6; Gaps 2;

QY 21 VLAQLDALLVFPQVQAQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYYRSEDHHRP 80
Db 3 MLTQPHSVESFGKTVISCTSDG--SIADSFVQVQYQRPGRAPTTVIF----DDNQRP 56

QY 81 ADIPDRFSAKDEAHNACVLTISVPQPEDDADYIC 115
Db 57 SGVPDRFSGSIDRSSNSASLTISGLQTEDEADYIC 91

RESULT 7
LV2F HUMAN STANDARD; PRT; 111 AA.
AC P01709;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region MGC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75013804; PubMed=4415202;
RA Fett J.W., Deutsch H.F.;
RT "Primary structure of the Mgc lambda chain.";
RL Biochemistry 13:4102-4114(1974).
RN [2]
RP LAMBDA CHAIN GENES.
RX MEDLINE=76093781; PubMed=812801;
RA Fett J.W., Deutsch H.F.;
RT "A new lambda-chain gene";
RL Immunochimistry 12:643-652(1975).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
Panagiotopoulos N.;
RT "Rotational allomerism and divergent evolution of domains in
immunoglobulin light chains";
RL Biochemistry 14:3953-3961(1975).
RN [4]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=90133913; PubMed=2515285;
RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT "Three-dimensional structure of a light chain dimer crystallized in
water. Conformational flexibility of a molecule in two crystal
forms";
RL J. Mol. Biol. 210:601-615(1989).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+

MARKERS.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A90381; L2HUMC.
DR PDB: 2MCG; 15-JUL-92.
DR PDB: 1A8J; 17-JUN-98.
DR PDB: 1DCU; 15-MAY-97.
DR GO: 0005576; C:extracellular; NAS.
DR GO: 0003823; F:antigen binding activity; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Hence-Jones protein; 3D-structure;
CW Pyroglutamate carboxylic acid.
PT DOMAIN 1 108
IG-LIKE.
PYROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
PT MOD RES 1 1
PT DISULFID 22 90
STRAND 5 5
STRAND 10 12
STRAND 18 23
TURN 26 32
STRAND 36 40
TURN 42 43
TURN 50 51
STRAND 52 54
TURN 55 55
STRAND 62 63
TURN 66 68
STRAND 72 77
STRAND 86 93
TURN 99 101
STRAND 105 109
TURN 111 111
NON TER 111
SEQUENCE 111 AA; 11558 MW; 70CID6E2FA3377BA CRC64;
Query Match 28.4%; Score 186.5; DB 1; Length 111;
Best Local Similarity 43.9%; Pred. No. 7.6e-13;
Matches 43; Conservative 16; Mismatches 32; Indels 7; Gaps 3;
DY 19 QTVLAQLDALLVFPQVAQISCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 78
DB 1 QSALTQPSASGSLGSLQSVTISCTGTSDVGNY-VSWYQQHAGKPKVIY----EVNK 55
QY 79 PADIPRFSAAKDEAHNACVLTISVPQEDDADYCS 116
DB 56 RPSGVDFRFGSK--SGNTASLTVSGLQADEADYCS 91
RESULT 8
LV2L_HUMAN STANDARD; PRT; 111 AA.
AC P80422;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma lambda chain V-II region DOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95252398; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monooxygenase
immunoglobulins".
RL Eur. J. Biochem. 228:886-893(1995).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP: P01709; 2MCG.

DR GO: 0005576; C:extracellular; NAS.
DR GO: 0003823; F:antigen binding activity; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 106
IG-LIKE.
BY SIMILARITY.
FT DISULFID 22 90
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11787 MW; F358B1EA2CD7109A CRC64;
Query Match 28.2%; Score 185.5; DB 1; Length 111;
Best Local Similarity 44.8%; Pred. No. 9.7e-13;
Matches 43; Conservative 14; Mismatches 32; Indels 7; Gaps 3;
QY 20 TVLAQLDALLVFPQVAQISCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 79
DB 2 SALTQPSLSGSGFQAVTISCTGLPS-VVDDNFVSWYQQTGPRAPRLIY---DDSLR 56
QY 80 PADIPRFSAAKDEAHNACVLTISVPQEDDADYCS 115
DB 57 PSCGVDFRFGSKSDTKAA--LTISGLQPDDEATYFC 90
RESULT 9
LV6D_HUMAN STANDARD; PRT; 111 AA.
AC P06318;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region WLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86122667; PubMed=4089539;
RA Dwalet F.B., Strako K., Benson M.D.;
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein
(WLT)".
RL Scand. J. Immunol. 22:653-660(1985).
DR PIR: A01989; L6HULT.
DR HSSP: P01709; 2MCG.
DR GO: 0005576; C:extracellular; NAS.
DR GO: 0003823; F:antigen binding activity; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 22
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 23 35
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 51 57
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 92 101
FRAMEWORK-4.
COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 102 111
BY SIMILARITY.
FT DISULFID 22 91
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE37BCE24F CRC64;
Query Match 28.2%; Score 185; DB 1; Length 111;
Best Local Similarity 45.2%; Pred. No. 1.1e-12;
Matches 38; Conservative 16; Mismatches 24; Indels 6; Gaps 2;

```

2Y 32 PQVQAQLSCTLPQHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIPDRFSAK 91
2D 14 PEKTVTISCTGSSG--SIGSNYYQVYQQRGAPTNTVII--ENNQRPEVDRFSGSI 67
2Y 92 DEAHNAVLTVISPVQPEDDADYYC 115
2D 68 DSSSNSASLTISGLKTEDEADYYC 91

RESULT 10
LV6E_HUMAN STANDARD; PRT; 131 AA.
AC P06319;
DT 01-JAN-1998 (Rel. 06, Created)
DT 01-JAN-1998 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 39, Last annotation update)
DE IG lambda chain V-VI region EB4 precursor.
CS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A. PubMed=3923440;
RX MEDLINE=85215660; PubMed=3923440;
RA Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT "Cloning and sequence analysis of an Ig lambda light chain mRNA
expressed in the Burkitt's lymphoma cell line EB4."
RL Nucleic Acids Res. 13:2931-2941(1985).
DR PIR; A01930; L6HUEB.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 131 IG LAMBDA CHAIN V-VI REGION EB4.
FT DOMAIN 20 41 FRAMEWORK-1.
FT DOMAIN 42 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 110 FRAMEWORK-3.
FT DOMAIN 111 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 131 FRAMEWORK-4.
FT DISULFID 41 110 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14147 MW; 02A9179C8C05C2CD CRC64;

Query Match 28.2%; Score 185; DB 1; Length 131;
Best Local Similarity 42.1%; Pred. No. 1.3e-12;
Matches 40; Conservative 16; Mismatches 33; Indels 6; Gaps 2;

QY 21 VLAQLDALLVFPQVQAQLSCTLPQHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHRRP 80
DB 22 MLTQPHSVESFGKVTITICT--GNSGSIASNYQVYQQRVSAPTIVY----EDNQR 75
QY 81 ADIPDRFSAKDEAHNAVLTVISPVQPEDDADYYC 115
DB 76 LGVPDRFSGSIDSSNSASLTISGLKTEDEADYYC 110

RESULT 11
LV2G_HUMAN STANDARD; PRT; 111 AA.
AC P01710;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region BO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE.
RX MEDLINE=71103825; PubMed=5532228;
RA Wikler M., Putnam F.W.;
RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
chymotryptic peptides, and sequence of protein Bo.";
RL J. Biol. Chem. 245:4488-4507(1970).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01976; L2HUBO.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyroglutamate carboxylic acid. IG-LIKE.
FT DOMAIN 1 106 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 28.1%; Score 184.5; DB 1; Length 111;
Best Local Similarity 41.8%; Pred. No. 1.2e-12;
Matches 41; Conservative 16; Mismatches 34; Indels 7; Gaps 3;

QY 19 QTVLAQLDALLVFPQVQAQLSCTLPQHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 78
DB 1 QSALTQPPSASGSGQSVTISCTSDVDGNKY-VSWYQQRGAPKLIVP----EVSQ 55
QY 79 RPADIPDRFSAKDEAHNAVLTVISPVQPEDDADYYCS 116
DB 56 RPSGVPDRFSGSKSD--NTASLTVSGLRADDEADYYCS 91

RESULT 12
LV1G_HUMAN STANDARD; PRT; 130 AA.
AC P06316;
DT 01-JAN-1998 (Rel. 06, Created)
DT 01-JAN-1998 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
sequence.";
RL Nucleic Acids Res. 12:8407-8414(1984).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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C  ENEL; X01147; CAA25598.1; -.
R  PIR; A01966; L1HUBU.
R  HSP; P01703; 7FAB.
R  GO; GO:0005576; C:extracellular; NAS.
R  GO; GO:0003823; F:antigen binding activity; NAS.
R  GO; GO:0006955; P:immune response; NAS.
R  InterPro; IPR007110; Ig-like.
R  InterPro; IPR003006; Ig_MHC.
R  InterPro; IPR003596; Ig_v.
R  Pfam; PF00047; Ig; 1.
R  SMART; SM00406; IGV; 1.
R  PROSITE; PS00835; IG_LIKE; 1.
R  Immunoglobulin V region; Signal.
C  SIGNAL 1 19 IG LAMBDA CHAIN V-I REGION BL2.
C  CHAIN 20 130 V SEGMENT.
C  DOMAIN 20 115 J SEGMENT.
C  DOMAIN 116 130 J SEGMENT.
C  DISULFID 41 108 BY SIMILARITY.
C  NON_TER 130 130
C  SEQUENCE 130 AA; 13564 MW; FA44BB17D3A55EBF CRC64;
Query Match 27.9%; Score 183.5; DB 1; Length 130;
Best Local Similarity 40.5%; Pred. No. 1.9e-12; Indels 9; Gaps 5;
Matches 47; Conservative 22; Mismatches 38;
Y  1 MACR-CISFLMGTFLSVSTVLAQLDALLVFPQVAQLSCTLSQPHVTIRDYGVSWYQQ 59
D  1 MTCSPLLTLLHCTGSAQSVLTQPPSVSAAPQKVITSCGSSNIG-NDY-VSWYQQ 58
Y  60 RAGSAPRYLYYSEEDHHPADIPRFSNAKDEAHNACVLITSPQEDDADYVC 115
D  59 VFGTAPKLLIY----DNKRPSGIPDRFSGSK--SGTSATLGLTGLTGDEADYVC 108

RESULT 13
LV2K HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani T., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RT Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
IMMUNOGLOBULINS. IV. Assignment of a subgroup.",
J. Biochem. 93:421-429(1983).
DE -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A01965; L1HUNG.
R  HSP; P01703; 7FAB.
R  GO; GO:0005576; C:extracellular; NAS.
R  GO; GO:0003823; F:antigen binding activity; NAS.
R  GO; GO:0006955; P:immune response; NAS.
R  InterPro; IPR007110; Ig-like.
R  InterPro; IPR003006; Ig_MHC.
R  InterPro; IPR003596; Ig_v.
R  Pfam; PF00047; Ig; 1.
R  SMART; SM00406; IGV; 1.
R  PROSITE; PS00835; IG_LIKE; 1.
R  Immunoglobulin V region; Pyrrolidone carboxylic acid.
C  DOMAIN 1 105 IG-LIKE.
C  MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
C  DISULFID 22 89 BY SIMILARITY.
C  NON_TER 111 111

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C  SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;
Query Match 27.5%; Score 180.5; DB 1; Length 111;
Best Local Similarity 41.1%; Pred. No. 3.3e-12; Indels 15; Gaps 4;
Matches 44; Conservative 19; Mismatches 29;
Y  19 QTVLAQLDALLVFPQVAQLSCTLSQPHVTIRDYGVSWYQQRAGSAPRYLYYSEEDH 78
D  1 QSVLTQPPSVSAAPQKVITSCGSSN--IGDNFVSWYQQLPGTAPKLLIY----DNK 54
Y  79 READIPDRFSAKDEAHNACVLITSPQEDDADYVC-----SVG 118
D  55 RPSGIPDRFSGSK--SGTSATLGLTGLTGDEADYVCCTWDSSLSVG 99

RESULT 14
LV2K HUMAN STANDARD; PRT; 112 AA.
AC P04209;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region NIG-84.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85204383; PubMed=3922791;
RA Tonolike H., Kametani T., Hoshi A., Shinoda T., Isobe T.;
RT "Amino acid sequence of an amyloidogenic Bence Jones protein in
myeloma-associated systemic amyloidosis.",
FEBS Lett. 185:139-141(1985).
DE -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A01971; L2HUNG.
R  HSP; P01709; 2MCG.
R  GO; GO:0005576; C:extracellular; NAS.
R  GO; GO:0003823; F:antigen binding activity; NAS.
R  GO; GO:0006955; P:immune response; NAS.
R  InterPro; IPR007110; Ig-like.
R  InterPro; IPR003006; Ig_MHC.
R  InterPro; IPR003596; Ig_v.
R  Pfam; PF00047; Ig; 1.
R  SMART; SM00406; IGV; 1.
R  PROSITE; PS00835; IG_LIKE; 1.
R  Immunoglobulin V region; Amyloid; Bence-Jones protein.
C  DOMAIN 1 102 IG-LIKE.
C  DISULFID 22 90 BY SIMILARITY.
C  NON_TER 112 112
C  SEQUENCE 112 AA; 11581 MW; 989FEF363AE1B4F3 CRC64;
Query Match 27.5%; Score 180.5; DB 1; Length 112;
Best Local Similarity 43.9%; Pred. No. 3.3e-12; Indels 7; Gaps 3;
Matches 43; Conservative 16; Mismatches 32;
Y  19 QTVLAQLDALLVFPQVAQLSCTLSQPHVTIRDYGVSWYQQRAGSAPRYLYYSEEDH 78
D  1 QSALTQPSVSGSFGQSITISCTGTTSDVGGYDF-VSWYQQHPGKAPKLLIY----DVNS 55
Y  79 RPADIPDRFSAKDEAHNACVLITSPQEDDADYVC 116
D  56 RPSGISNRFSGSK--SGNTASLTISGLQABDEADYVC 91

RESULT 15
LV2K HUMAN STANDARD; PRT; 117 AA.
AC P04211;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
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Search completed: February 9, 2004, 12:47:04
Job time : 11.6351 secs

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W protein - protein search, using sw model

run on: February 9, 2004, 12:38:06 ; Search time 38.7838 seconds
(without alignments)
818.395 Million cell updates/sec

Title: US-09-981-876-200

Perfect score: 657

Sequence: 1 MACRCLSLMGTFLSVSQT.....PVQPEDDADYCVSGVGFSP 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

1: sp_arChea:*

2: sp_Bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	430	65.4	123	11	Q61243	Q61243 mus musculus
2	199	30.3	112	4	Q96JD1	Q96JD1 homo sapien
3	199	30.3	135	4	Q9H5Z4	Q9H5Z4 homo sapien
4	194	29.5	112	4	Q96JD2	Q96JD2 homo sapien
5	191.5	29.1	116	4	Q96JD0	Q96JD0 homo sapien
6	190.5	29.0	236	4	Q96E61	Q96E61 homo sapien
7	187	28.5	237	4	Q9WTU6	Q9WTU6 homo sapien
8	184.5	28.1	237	4	Q9WUK4	Q9WUK4 homo sapien
9	182	27.7	240	4	Q9WUK3	Q9WUK3 homo sapien
10	178	27.1	234	4	Q9N355	Q9N355 homo sapien
11	174	26.5	235	11	Q99M11	Q99M11 mus musculus
12	171	26.0	107	4	Q9NSD6	Q9NSD6 homo sapien
13	170	25.9	233	4	Q9TBC9	Q9TBC9 homo sapien
14	169.5	25.8	236	4	Q9NEJ1	Q9NEJ1 homo sapien
15	168	25.6	108	4	Q96SB0	Q96SB0 homo sapien
16	167.5	25.5	109	4	Q9UL86	Q9UL86 homo sapien

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17 166 25.3 100 6 077624
18 166 25.3 110 4 08TE63
19 164 25.0 233 4 096I69
20 164 25.0 233 4 08N5F4
21 159.5 24.3 109 4 08UL78
22 158.5 24.1 105 4 08WJ36
23 154.5 23.5 132 4 08TBD0
24 154 23.4 107 4 09UL82
25 151 23.0 101 4 08IZD8
26 140.5 21.4 108 4 09UL83
27 140.5 21.4 234 4 08NEK1
28 136.5 20.8 484 11 08VEA0
29 136 20.7 129 11 08VDE2
30 135.5 20.6 109 4 09UL85
31 135.5 20.6 113 11 08CGS1
32 134 20.4 97 4 043234
33 134 20.4 107 11 09ERZ9
34 134 20.4 235 11 091WI2
35 133.5 20.3 93 4 09UL76
36 131 19.9 239 4 08NEK0
37 130.5 19.9 99 11 09UL74
38 130.5 19.9 108 4 09UL79
39 129 19.6 134 11 08VDD0
40 128 19.5 107 4 096SA9
41 128 19.5 108 4 09UL77
42 126.5 19.3 521 4 08N4Y9
43 126 19.2 278 11 0921K1
44 126 19.2 468 11 099L31
45 125.5 19.1 111 11 0920E9

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ALIGNMENTS

RESULT 1

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ID Q61243 PRELIMINARY; PRT; 123 AA.
AC Q61243;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE 8S20 protein precursor (Pre-B lymphocyte gene 3).
GN VPB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=93259124; PubMed=8491176;
RA Shirasawa T., Ohnishi K., Hagiwara S., Shigemoto K., Takebe Y.,
RA Rajewsky K., Takemori T.;
RT "A novel gene product associated with mu chains in immature B cells.";
RL EMBL J. 12:1827-1834(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okkido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; D13208; BAA02495.1; -.
DR EMBL; AK008794; BAE25899.1; -.
DR HSSP; P01709; 2MCG.
DR MGD; MGI:98938; Vpreb3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT CHAIN 20..123
FT PROTEIN 1..8520 PROTEIN.
SQ SEQUENCE 123 AA; 13400 MW; 2A1AD371D1CEE98F CRC64;

Query Match 65.4%; Score 430; DB 11; Length 123;
Best Local Similarity 66.1%; Pred. No. 5.7e-41;
Matches 82; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

QY 1 MAC-RCLFLLMGTLFVSQVTLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQ 59
DB 1 MACPGCLLELLTGTFVAVFQPTLTQPDASFVFPQGDALHLSCTINSQATAGDIGVSWYQQ 60
QY 60 RAGSAPRYLLYRSBEDHRRPADIPDRFSAKDAHNACVLTISPVQEDADYICVGY 119
DB 61 QGGSAP-HLLYYABEHRPADIPDRFSATVDAHNACILITISPLPDDADYFCGSI 119
QY 120 GFSP 123
DB 120 TREP 123

RESULT 2
Q96JD1 PRELIMINARY; PRT; 112 AA.
ID Q96JD1
AC Q96JD1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid lambda 6 light chain variable region PIP (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Bone marrow;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267874; AAK58586.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 112
SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match 30.3%; Score 199; DB 4; Length 112;
Best Local Similarity 44.2%; Pred. No. 8.5e-15;
Matches 42; Conservative 17; Mismatches 30; Indels 6; Gaps 2;

QY 21 VLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQAGSAPRYLLYRSBEDHRRP 80
DB 3 MLTQFHSVSPGKTIITISCTRSSG--SIASNYVQYQRPQSGAPTIVY----EDNQRP 56
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QY 81 ADIPDRFSAKDAHNACVLTISPVQEDADYIC 115
DB 57 SGVDFRFGSSIDSSNSASLTISGLKTEADYIC 91

RESULT 3
Q9HSZ4 PRELIMINARY; PRT; 135 AA.
ID Q9HSZ4
AC Q9HSZ4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ22755.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=ileal mucosa;
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026408; BAB15473.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR Hypothetical protein.
KW SEQUENCE 135 AA; 14780 MW; 652492DED930F401 CRC64;

Query Match 30.3%; Score 199; DB 4; Length 135;
Best Local Similarity 45.3%; Pred. No. 1.1e-14;
Matches 34; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 48 TIRYGVSWYQAGSAPRYLLYRSBEDHRRPADIPDRFSAKDAHNACVLTISPVQ 107
DB 7 SVGDFTIRWYQKGNPRVLLYHSDNKGQSGVPSRFGSGNSANAGILIRISGLQ 66
QY 108 EDDADYICVSGYGF 122
DB 67 EDEADYICGTWHSN 81

RESULT 4
Q96JD2 PRELIMINARY; PRT; 112 AA.
ID Q96JD2
AC Q96JD2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid lambda 6 light chain variable region NEG (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Bone marrow;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267873; AAK58585.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
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Db 61 RSPQYIMKVKSDGSHNGKDGIPIDRFWGSSGADR--YLTTSLNQSDDEAEYHCGESHTID 118

QY 116 -SVGYGF 121
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Db 119 GQGVWF 125

RESULT 10
QB355 PRELIMINARY; PRT; 234 AA.

ID QB355;
AC QB355;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP STRAUSBERG R.;
RC TISSUE=Brain;
RA Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RL EMBL; BC028090; AAB28090.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;

Query Match 27.1%; Score 178; DB 4; Length 234;
Best Local similarity 38.1%; Pred. No. 5e-12; Indels 14; Gaps 4;
Matches 44; Conservative 18; Mismatches 37;

QY 9 LLMGTFLL---SVSOTVLAQLDALLVPFGQVAQLSCTLSPQHVTIRDVGSWYQQPAGSA 64
|||:
Db 6 LLLGLLSHCTGVSIVTLTPPSVSPVAGQTARITCGN----NIGSKSVHWYQQKPQGA 61
|||:

QY 65 PYVLLYRSEEDHHRPADIPRFSAAXDEAHNAVCVLTISPVQPEDDDADYCVS 117
:|||:
Db 62 FVLVVY---DDSDRPSGIPERFSGS--NSGNATLTISRVDAGDEADYYCQL 108
:|||:

RESULT 11
QB355 PRELIMINARY; PRT; 235 AA.

ID QB355;
AC QB355;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JAN-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 25.4 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAUSBERG R.;
RC Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RL EMBL; BC002129; AAA02129.1; -;
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.

```
R SMART; SM00406; IGV; 1.
R PROSITE; PS00290; IG_MHC; 1.
W Hypothetical protein.
Q SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 26.5%; Score 174; DB 11; Length 235;
Best Local Similarity 40.0%; Pred. No. 1.4e-11;
Matches 40; Conservative 16; Mismatches 38; Indels 6; Gaps 2;

Y 16 SVSQTVLQDALLVFPQVQAQLSCTLSPPQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHH 75
b 17 SCAQLVLTQPSVSTSLGAKLPKASTGN--IGDSYNNWYQVMGRSPNMIY-----G 70
Y 76 DHRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYYC 115
b 71 DDLRPGSVDRSGSIDSSNGAFLTIQNVQADDEADYYC 110

RESULT 12
Q8NSD6 PRELIMINARY; PRT; 107 AA.
C Q8NSD6;
T 01-OCT-2000 (T-EMBLrel. 15, Created)
T 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
T 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
XN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
LA Hohmann A.;
IL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
JR EMBL; I43092; AAA69746.2; --
JR HSPF; P01709; 2MCG.
JR InterPro; IPR007110; Ig-like.
JR InterPro; IPR003006; IG_MHC.
JR InterPro; IPR003596; IG_V.
JR Pfam; PF00047; Ig; 1.
JR SMART; SM00406; IGV; 1.
JR PROSITE; PS50835; IG_LIKE; 1.
JT NON_TER
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 26.0%; Score 171; DB 4; Length 107;
Best Local Similarity 40.0%; Pred. No. 1.2e-11;
Matches 38; Conservative 18; Mismatches 29; Indels 10; Gaps 3;

QY 22 LAQLDALLVFPQVQAQLSCTLSPPQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHHPA 81
DB 2 LTQDPVWSVALGQVTRITC-----QGSLSRYASWYQKQEQAPVLVIYK-----NNRPS 53
QY 82 DIPDRFSAKDEAHNACVLTISPVPQEDDADYYCS 116
DB 54 GIPDRFSGS--SSGNWASLTITGAQADEADYYCN 86

RESULT 13
Q8TBC9 PRELIMINARY; PRT; 233 AA.
AC Q8TBC9;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RC TISSUE=B-Cell;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; SC02823; AAH22823.1; --
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;

Query Match 25.9%; Score 170; DB 4; Length 233;
Best Local Similarity 40.2%; Pred. No. 4.1e-11;
Matches 39; Conservative 17; Mismatches 25; Indels 16; Gaps 4;

QY 22 LAQLDALLVFPQVQAQLSCT--LSPQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHH 78
DB 23 LTQPPSVSVSPQVTRITCSGDALPKQY-----AYWYQKQEQAPVLVIY---KDNE 71
QY 79 RPADIPDRFSAKDEAHNACVLTISPVPQEDDADYYC 115
DB 72 RPSGIPERFSGS--SSGTTVLTITSGVQAEDADYYC 106

RESULT 14
Q8NEJ1 PRELIMINARY; PRT; 236 AA.
AC Q8NEJ1;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
XN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 25.8%; Score 169.5; DB 4; Length 236;
Best Local Similarity 40.4%; Pred. No. 4.7e-11;
Matches 46; Conservative 23; Mismatches 32; Indels 13; Gaps 6;

QY 8 FLNGTEL-----SVSQTVLAQLDALLVFPQVQAQLSCTLSPPQHVITRDYGVSWYQORAG 62
DB 4 FPLLTLTLTTCAGSNAQSVLTQPPSAGSGPQGVITISCGSRNIG-SNY-VYVYQVPG 61
QY 63 SAPRYLLYRSEEDHHPADIPDRFSAKDEAHNACVLTISPVPQEDDADYYCS 116
DB 62 TAPK-LLIYRNDQ---RPSGVDRFSGSK--SGTSASLAISGLRSEADYYTCA 109

RESULT 15
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Q96SBO
ID Q96SBO PRELIMINARY; PRT; 108 AA.
AC Q96SBO;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin lambda light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=9712075;
RX MEDLINE=98375893; Shikman A.K., Ward K.E., Cunningham M.W.;
RA "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96394; AAB68783.1; -;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;
Query Match 25.6%; Score 168; DB 4; Length 108;
Best Local Similarity 39.8%; Pred.No.2.7e-11;
Matches 39; Conservative 21; Mismatches 30; Indels 8; Gaps 4;
QY 19 QTVLAQLDALLVPPGVAQLSCTLSPQHVITRDYGVSWYQORAGSAPRYLLYYRSEEDHH 78
Db 1 QSVLTQPPSASGTPQRTVITSCGSSNIG-SNY-VWYQQLPGTAPKLLIY---RNNQ 54
QY 79 RPADIPDRFSAKDEAHNACVLTITSPVOPEDDADYICS 116
Db 55 RPSGVDPDRFSGK--SGTSASLAISGLRSEDEADYICA 90

Search completed: February 9, 2004, 12:48:28
Job time : 41.7838 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: February 9, 2004, 08:36:32 ; Search time 38.2297 Seconds
(without alignments)
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file: US-09-981-876-200

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- 12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
- 13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
- 14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
- 15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
- 16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
- 17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
- 18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
- 19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	657	100.0	123	AAW75123	Human secreted pro
2	657	100.0	123	AAE24061	Human PRO619 prote
3	657	100.0	123	AAE66855	Membrane-bound pro
4	657	100.0	123	AAU12372	Human PRO619 polyp
5	657	100.0	123	AAE65178	Human PRO619 (UNQ3
6	657	100.0	123	AAU66770	Human PRO polypept
7	657	100.0	123	AAU67046	Human secreted/tra
8	657	100.0	123	ABU59851	Novel secreted and
9	657	100.0	123	ABU59071	Novel human secret

10	657	100.0	123	24	ABU59218	Human secreted/tra
11	657	100.0	123	24	ABU59367	Novel human secret
12	657	100.0	123	24	ABU60502	Human secreted/tra
13	657	100.0	123	24	ABU57993	Human PRO polypept
14	657	100.0	123	24	ABU58924	Human secreted/tra
15	657	100.0	123	24	ABU13884	Human PRO619 polyp
16	657	100.0	123	24	ABU10839	Human PRO polypept
17	634	96.5	141	22	AAU39690	Human polypeptide
18	582	88.6	113	22	AAU41476	Human polypeptide
19	251.5	38.3	182	22	ABG19759	Novel human diagno
20	244.5	37.2	185	22	ABG29426	Novel human diagno
21	236	35.9	256	23	ABP45219	Human Blys binding
22	234	35.6	259	23	ABP45474	Human Blys binding
23	233.5	35.5	237	22	ABG19300	Novel human diagno
24	233.5	35.5	250	22	ABG19303	Novel human diagno
25	232.5	35.4	277	22	ABG19760	Novel human diagno
26	231.5	35.2	142	9	AAU83001	V preB-2 protein.
27	227.5	34.6	142	9	AAU83008	V preB-1 protein.
28	227	34.6	259	23	ABP45541	Human Blys binding
29	225	34.2	263	23	ABP45267	Human Blys binding
30	217.5	33.1	105	22	ABG22849	Novel human diagno
31	208.5	31.7	542	22	ABG23085	Novel human diagno
32	207.5	31.6	244	22	ABG19289	Novel human diagno
33	206.5	31.4	137	19	AAU57597	Chimeric antibody
34	206.5	31.4	137	20	AAU89641	Human antibody hMB
35	206.5	31.4	137	21	AAU77525	Peptide encoded by
36	206.5	31.4	137	22	AAU67106	Amino acid sequenc
37	206.5	31.4	137	22	AAU63404	Amino acid sequenc
38	206.5	31.4	137	22	AAU63405	Humanised anti-PTH
39	206.5	31.4	137	22	AAU64787	Human joint diseas
40	206.5	31.4	137	23	ABU95214	Arginogenesis inhib
41	206.5	31.4	138	24	ABU36673	Human Vpre-B prote
42	205	31.2	125	9	AAU80289	Human VSGF-2 relat
43	204	31.1	248	24	ABU19832	Chimeric antibody
44	203.5	31.0	137	19	AAU57598	Chimeric antibody
45	203.5	31.0	137	19	AAU57595	Chimeric antibody

ALIGNMENTS

RESULT 1
AAW75123
ID AAW75123 standard; Protein; 123 AA.
XX AC AAW75123;
XX AC AAW75123;
XX DT 25-MAR-2003 (updated)
XX DT 28-JAN-1999 (first entry)
XX DE Human secreted protein encoded by gene 67 clone HRGDF73.
XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX KW diagnosis; tissue; cancer; tumor; neurodegenerative disorder; leukaemia;
XX KW developmental abnormality; foetal deficiency; blood; allergy; renal;
XX KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX OS Homo sapiens.
XX FN WO9839446-A2.
XX PD 11-SEP-1998.
XX PF 06-MAR-1998; 98WO-US04482.
XX PR 07-MAR-1997; 97US-0038621.
XX PR 07-MAR-1997; 97US-0040161.
XX PR 07-MAR-1997; 97US-0040162.
XX PR 07-MAR-1997; 97US-0040163.

PR 07-MAR-1997; 97US-0040333.
 PR 07-MAR-1997; 97US-0040334.
 PR 07-MAR-1997; 97US-0040336.
 PR 07-MAR-1997; 97US-0040626.
 PR 11-APR-1997; 97US-0043311.
 PR 11-APR-1997; 97US-0043312.
 PR 11-APR-1997; 97US-0043313.
 PR 11-APR-1997; 97US-0043314.
 PR 11-APR-1997; 97US-0043315.
 PR 11-APR-1997; 97US-0043568.
 PR 11-APR-1997; 97US-0043569.
 PR 11-APR-1997; 97US-0043576.
 PR 11-APR-1997; 97US-0043578.
 PR 11-APR-1997; 97US-0043580.
 PR 11-APR-1997; 97US-0043669.
 PR 11-APR-1997; 97US-0043670.
 PR 11-APR-1997; 97US-0043671.
 PR 11-APR-1997; 97US-0043672.
 PR 11-APR-1997; 97US-0043674.
 PR 23-MAY-1997; 97US-0047492.
 PR 23-MAY-1997; 97US-0047500.
 PR 23-MAY-1997; 97US-0047501.
 PR 23-MAY-1997; 97US-0047502.
 PR 23-MAY-1997; 97US-0047503.
 PR 23-MAY-1997; 97US-0047581.
 PR 23-MAY-1997; 97US-0047582.
 PR 23-MAY-1997; 97US-0047583.
 PR 23-MAY-1997; 97US-0047584.
 PR 23-MAY-1997; 97US-0047585.
 PR 23-MAY-1997; 97US-0047586.
 PR 23-MAY-1997; 97US-0047587.
 PR 23-MAY-1997; 97US-0047588.
 PR 23-MAY-1997; 97US-0047589.
 PR 23-MAY-1997; 97US-0047590.
 PR 23-MAY-1997; 97US-0047592.
 PR 23-MAY-1997; 97US-0047593.
 PR 23-MAY-1997; 97US-0047594.
 PR 23-MAY-1997; 97US-0047595.
 PR 23-MAY-1997; 97US-0047596.
 PR 23-MAY-1997; 97US-0047597.
 PR 23-MAY-1997; 97US-0047598.
 PR 23-MAY-1997; 97US-0047599.
 PR 23-MAY-1997; 97US-0047600.
 PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.
 PR 22-AUG-1997; 97US-0056630.
 PR 22-AUG-1997; 97US-0056631.
 PR 22-AUG-1997; 97US-0056632.
 PR 22-AUG-1997; 97US-0056636.
 PR 22-AUG-1997; 97US-0056637.
 PR 22-AUG-1997; 97US-0056662.
 PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056864.
 PR 22-AUG-1997; 97US-0056872.
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 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.

PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 05-SEP-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057761.

(HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC, Bednarek DP;
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
 PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

XX WPI; 1998-609887/51.

DR N-PSDB; AAV34220.

XX New isolated human genes and the secreted polypeptides they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders

XX Claim 1; Page 320-321; 447pp; English.

XX This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line.
 CC The gene can be used to generate fusion proteins by linking to the gene
 CC to a human immunoglobulin Fc portion (e.g. AAV34145), for increasing the
 CC stability of the fused protein as compared to the human protein only.
 CC The invention relates to 70 novel genes and their fragments (nucleic
 CC acid sequences: AAV34154-V34276; amino acid sequences AAV75057-W75179)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 70
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV34154 for described uses).
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 19; Length 123;

Best Local Similarity 100.0%; Pred. NO. 5.9e-65;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MACRCLSFLLMGTFLSVSTQVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60

DB 1 MACRCLSFLLMGTFLSVSTQVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60

OY 61 AGSAPRYLLYRSEEDHRRPADIPDRPSAAKDEAHNACVLTISFVQPEDDADYCSGVYG 120

DB 61 AGSAPRYLLYRSEEDHRRPADIPDRPSAAKDEAHNACVLTISFVQPEDDADYCSGVYG 120

OY 121 FSP 123

DB 121 FSP 123

RESULT 2

AA524061

ID AAB24061 standard; Protein; 123 AA.

XX

PR	17-JUN-1998;	98US-0089532.
PR	17-JUN-1998;	98US-0089538.
PR	17-JUN-1998;	98US-0089598.
PR	17-JUN-1998;	98US-0089599.
PR	17-JUN-1998;	98US-0089600.
PR	17-JUN-1998;	98US-0089653.
PR	18-JUN-1998;	98US-0089801.
PR	18-JUN-1998;	98US-0089907.
PR	18-JUN-1998;	98US-0089908.
PR	19-JUN-1998;	98US-0089947.
PR	19-JUN-1998;	98US-0089948.
PR	19-JUN-1998;	98US-0089952.
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PR	22-JUN-1998;	98US-0090252.
PR	22-JUN-1998;	98US-0090254.
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PR	24-JUN-1998;	98US-0090429.
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PR	25-JUN-1998;	98US-0090694.
PR	25-JUN-1998;	98US-0090695.
PR	25-JUN-1998;	98US-0090696.
PR	26-JUN-1998;	98US-0090862.
PR	26-JUN-1998;	98US-0090863.
PR	01-JUL-1998;	98US-0091358.
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PR	01-JUL-1998;	98US-0091544.
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PR	02-JUL-1998;	98US-0091626.
PR	02-JUL-1998;	98US-0091628.
PR	02-JUL-1998;	98US-0091633.
PR	02-JUL-1998;	98US-0091646.
PR	02-JUL-1998;	98US-0091673.
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PR	07-JUL-1998;	98US-0092182.
PR	09-JUL-1998;	98US-0092472.
PR	10-JUL-1998;	98US-0093339.
PR	20-JUL-1998;	98US-0094651.
PR	04-AUG-1998;	98US-0095282.
PR	04-AUG-1998;	98US-0095285.
PR	04-AUG-1998;	98US-0095301.
PR	04-AUG-1998;	98US-0095302.
PR	04-AUG-1998;	98US-0095318.
PR	04-AUG-1998;	98US-0095321.
PR	04-AUG-1998;	98US-0095325.
PR	10-AUG-1998;	98US-0095916.
PR	10-AUG-1998;	98US-0095929.
PR	10-AUG-1998;	98US-0096012.
PR	11-AUG-1998;	98US-0096143.
PR	11-AUG-1998;	98US-0096146.
PR	12-AUG-1998;	98US-0096329.
PR	17-AUG-1998;	98US-0096757.
PR	17-AUG-1998;	98US-0096766.
PR	17-AUG-1998;	98US-0096768.
PR	17-AUG-1998;	98US-0096773.
PR	17-AUG-1998;	98US-0096791.
PR	17-AUG-1998;	98US-0096867.
PR	17-AUG-1998;	98US-0096891.
PR	17-AUG-1998;	98US-0096894.
PR	17-AUG-1998;	98US-0096895.
PR	17-AUG-1998;	98US-0096897.
PR	18-AUG-1998;	98US-0096949.
PR	18-AUG-1998;	98US-0096950.
PR	18-AUG-1998;	98US-0096959.
PR	18-AUG-1998;	98US-0096960.
PR	18-AUG-1998;	98US-0097022.
PR	19-AUG-1998;	98US-0097141.
PR	20-AUG-1998;	98US-0097218.
PR	24-AUG-1998;	98US-0097661.
PR	26-AUG-1998;	98US-0097951.
PR	26-AUG-1998;	98US-0097952.
PR	26-AUG-1998;	98US-0097954.
PR	26-AUG-1998;	98US-0097955.
PR	26-AUG-1998;	98US-0097971.
PR	26-AUG-1998;	98US-0097974.
PR	26-AUG-1998;	98US-0097978.
PR	26-AUG-1998;	98US-0097979.
PR	26-AUG-1998;	98US-0097986.
PR	26-AUG-1998;	98US-0098014.
PR	31-AUG-1998;	98US-0098525.
PR	16-SEP-1998;	98US-0100634.
PR	12-JAN-1999;	99US-0115565.
XX	(GETH) GENENTECH INC.	
PA	Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;	
PI	Wood WL, Yuan J;	
XX	WPI; 2000-072883/06.	
DR	N-PSDB; AAZ64983.	
XX	Membrane-bound proteins and related nucleotide sequences	
PT	claim 12; Fig 68; 822pp; English.	
XX	The invention provides membrane-bound PRO polypeptides and	
CC	polynucleotides encoding them. The PRO sequences of the invention were	
CC	identified based on extracellular domain homology screening. The PRO	
CC	sequences have homology with proteins including LDL receptors, TIE	
CC	ligands and various enzymes. The membrane-bound proteins and receptor	
CC	molecules are useful as pharmaceutical and diagnostic agents. Receptor	
CC	immunoadhesins, for instance, can be used as therapeutic agents to block	
CC	receptor-ligand interactions. The membrane-bound proteins can also be	
CC	employed for screening of potential peptide or small molecule inhibitors	
CC	of the relevant receptor/ligand interaction. The PRO encoding sequences	
CC	are useful as hybridization probes in chromosome and gene mapping and in	
CC	the generation of antisense RNA and DNA. PRO nucleic acid sequences	
CC	will also be useful for the preparation of PRO polypeptides, especially	
CC	by recombinant techniques.	
XX	Sequence 123 AA;	
SQ	Query Match 100.0%; Score 657; DB 21; Length 123;	
	Best Local Similarity 100.8%; Pred. No. 5.9e-65;	
	Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MACRCLSFLLMGTFSLVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSYQQR 60	
DB	1 MACRCLSFLLMGTFSLVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSYQQR 60	
QY	61 AGSAPRYLLYYRSEDDHRRPADIDRFSAKDEAHNAACVLTISPQVEDDADYYCSVGYG 120	
DB	61 AGSAPRYLLYYRSEDDHRRPADIDRFSAKDEAHNAACVLTISPQVEDDADYYCSVGYG 120	
QY	121 FSP 123	
DB	121 FSP 123	

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RESULT 4
AAU12372
ID AAU12372 standard; Protein; 123 AA.
XX
AC AAU12372;
XX
JT 24-OCT-2001 (first entry)
XX
JE Human PRO619 polypeptide sequence.
XX
CW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
CW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
CW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
CW adipocyte; A-peptide; factor VIIA; gene therapy.
XX
DS Homo sapiens.
XX
PN WO2000140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28531.
PR 02-DEC-1999; 99WO-US28584.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05084.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AA521444.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical.
XX
PS Claim 12; Fig 402; 813pp; English.
XX
AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO

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CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 123 AA;
Query Match 100.0%; Score 657; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MACRCLSFLLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60
Db 1 MACRCLSFLLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60
Qy 61 AGSAPRYLLYRSEEDHHRPADIPORFSAKDEAHNACVLTISPQPEDDADYYCSGVG 120
Db 61 AGSAPRYLLYRSEEDHHRPADIPORFSAKDEAHNACVLTISPQPEDDADYYCSGVG 120
Qy 121 FSP 123
Db 121 FSP 123
RESULT 5
AAB65178
ID AAB65178 standard; Protein; 123 AA.
XX
AC AAB65178;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO619 (UNQ355) protein sequence SEQ ID NO:117.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 08-OCT-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.

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PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 02-MAR-2000; 2000WO-US05004.
PR 15-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX (GETH) GENENTECH INC.
PA
XX PI Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL,
XX PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX WPI: 2001-032160/04.
DR N-PSDB; AAF44129.
XX
XX PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
PT
XX Claim 12; Fig 68; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB55154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 123 AA;
Query Match 100.0%; Score 657; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MACRCLSLFMGTFLVSQTVLAQLDALLVFPQVQVQLSCTLSFQVHTIRDYGVSYQQR 60
DB 1 MACRCLSLFMGTFLVSQTVLAQLDALLVFPQVQVQLSCTLSFQVHTIRDYGVSYQQR 60
QY 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISPVQEDDADYYCVSYG 120
DB 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISPVQEDDADYYCVSYG 120
QY 121 FSP 123
DB 121 FSP 123
RESULT 6
ABU66770
ID ABU66770 standard; Protein; 123 AA.
XX
XX AC ABU66770;
XX
XX 23-MAY-2003 (first entry)
DE Human PRO polypeptide #201.
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytostatic.

XX OS Homo sapiens.
XX PN US2003036180-A1.
XX PD 20-FEB-2003.
XX
XX 09-MAY-2002; 2002US-0143114.
XX
XX 31-MAR-1997; 97WO-US05230.
XX 12-JUN-1998; 98WO-US12456.
XX 14-JUL-1998; 98WO-US14552.
XX 28-AUG-1998; 98WO-US17888.
XX 10-SEP-1998; 98WO-US18824.
XX 14-SEP-1998; 98WO-US19033.
XX 14-SEP-1998; 98WO-US19094.
XX 14-SEP-1998; 98WO-US19177.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 07-OCT-1998; 98WO-US21141.
XX 29-OCT-1998; 98WO-US22991.
XX 29-OCT-1998; 98WO-US22992.
XX 20-NOV-1998; 98WO-US24855.
XX 01-DEC-1998; 98WO-US25108.
XX 05-JAN-1999; 99WO-US00106.
XX 08-MAR-1999; 99WO-US05028.
XX 10-MAR-1999; 99WO-US05190.
XX 20-APR-1999; 99WO-US08615.
XX 14-MAY-1999; 99WO-US10733.
XX 02-JUN-1999; 99WO-US12252.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 29-NOV-1999; 99WO-US28214.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 16-DEC-1999; 99WO-US28565.
XX 20-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 22-DEC-1999; 99WO-US30999.
XX 22-DEC-1999; 99WO-US30720.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 11-FEB-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 01-MAR-2000; 2000WO-US05601.
XX 02-MAR-2000; 2000WO-US05746.
XX 02-MAR-2000; 2000WO-US05841.
XX 10-MAR-2000; 2000WO-US06319.
XX 15-MAR-2000; 2000WO-US06884.
XX 20-MAR-2000; 2000WO-US07377.
XX 21-MAR-2000; 2000WO-US07532.
XX 30-MAR-2000; 2000WO-US08439.
XX 17-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US15264.
XX 28-JUL-2000; 2000WO-US20710.
XX 11-AUG-2000; 2000WO-US22031.

23-AUG-2000; 2000WO-US23522.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
10-NOV-2000; 2000WO-US30873.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-MAR-2001; 2001WO-US06666.
25-MAY-2001; 2001WO-US17092.
01-JUN-2001; 2001WO-US17800.
22-JUN-2001; 2001WO-US19692.
22-JUN-2001; 2001WO-US20116.
29-JUN-2001; 2001WO-US21066.
09-JUL-2001; 2001WO-US21735.
20-DEC-2000; 2000US-0747253.
28-FEB-2001; 2001US-0796498.
09-MAR-2001; 2001US-0802706.
14-MAR-2001; 2001US-0806889.
22-MAR-2001; 2001US-0816744.
05-APR-2001; 2001US-0828366.
10-MAY-2001; 2001US-0854208.
10-MAY-2001; 2001US-0854280.
18-MAY-2001; 2001US-0860216.
25-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
01-JUN-2001; 2001US-0872035.
05-JUN-2001; 2001US-0874503.
14-JUN-2001; 2001US-0882636.
19-JUN-2001; 2001US-0886342.
21-JUN-2001; 2001US-0887879.
18-JUL-2001; 2001US-0908827.
06-AUG-2001; 2001US-0924419.
09-AUG-2001; 2001US-0927796.
16-AUG-2001; 2001US-0931836.
19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2003-332040/31.
N-PSDB; ACA03803.

New secreted and transmembrane PRO nucleic acids, useful for gene
therapy, in chromosome and gene mapping, as chromosome markers, in
tissue typing, and in chromosome identification

Claim 12; Fig 402; 60pp; English.

The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The
PRO polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for
linking bioactive molecules to cells expressing PRO polypeptides,
for modulating biological activities of cells expressing PRO
polypeptides, and for identifying agonists or antagonists.
The PRO polypeptides are useful for stimulating the release of
tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
proliferation or differentiation of chondrocytes, and detecting the
presence of tumours. The polynucleotide sequences encoding PRO
polypeptides are useful as hybridisation probes, in chromosome and
gene mapping, in the generation of antisense RNA and DNA, in the
preparation of PRO polypeptides, for generating transgenic animals or
knockout animals, for the genetic analysis of individuals with genetic
disorders, and in gene therapy. ABU6570-ABU66844 represent the human
PRO polypeptides of the invention.
Note: The sequence data for this patent was obtained in electronic
format directly from the USPTO web site at
seqdata.uspto.gov/psipdsIDEntry.html.

Sequence 123 AA;

Query Match 100.0%; Score 657; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0;
QY 1 MACRCISFLLMGTFLSVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSWYQQR 60
DB 1 MACRCISFLLMGTFLSVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSWYQQR 60
QY 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYCVSYG 120
DB 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYCVSYG 120
QY 121 FSP 123
DB 121 FSP 123

RESULT 7

ABU67046
ID ABU67046 standard; Protein; 123 AA.

XX AC ABU67046;

XX DT 27-MAY-2003 (first entry)

XX DE Human secreted/transmembrane, PRO, protein SEQ ID 402.

XX KW Human, secreted protein; transmembrane protein; PRO;
XX KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
XX KW infertility; birth defects; premature aging; AIDS; biosensor;
XX KW acquired immunodeficiency syndrome; cancer; diabetic complication;
XX KW bioreactor; tumour.

XX OS Homo sapiens.

XX PN US2003032155-A1.

XX PD 13-FEB-2003.

XX PF 03-MAY-2002; 2002US-0137865.

XX PR 31-MAR-1997; 97WO-US05230.
XX PR 12-JUN-1998; 98WO-US12456.
XX PR 14-JUL-1998; 98WO-US14552.
XX PR 28-AUG-1998; 98WO-US17888.
XX PR 10-SEP-1998; 98WO-US18824.
XX PR 14-SEP-1998; 98WO-US19094.
XX PR 14-SEP-1998; 98WO-US19177.
XX PR 16-SEP-1998; 98WO-US19330.
XX PR 17-SEP-1998; 98WO-US19437.
XX PR 07-OCT-1998; 98WO-US21141.
XX PR 29-OCT-1998; 98WO-US22991.
XX PR 29-OCT-1998; 98WO-US22992.
XX PR 20-NOV-1998; 98WO-US24855.
XX PR 01-DEC-1998; 98WO-US25108.
XX PR 05-JAN-1999; 99WO-US00106.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 10-MAR-1999; 99WO-US05190.
XX PR 20-APR-1999; 99WO-US08615.
XX PR 14-MAY-1999; 99WO-US10733.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 08-SEP-1999; 99WO-US20594.
XX PR 13-SEP-1999; 99WO-US20944.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 15-SEP-1999; 99WO-US21547.
XX PR 05-OCT-1999; 99WO-US23089.
XX PR 29-NOV-1999; 99WO-US28214.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 30-NOV-1999; 99WO-US28409.
XX PR 01-DEC-1999; 99WO-US28301.

PR	01-DEC-1999;	99WO-US28634.
PR	02-DEC-1999;	99MO-US28551.
PR	02-DEC-1999;	99MO-US28554.
PR	02-DEC-1999;	99MO-US28565.
PR	16-DEC-1999;	99MO-US28565.
PR	20-DEC-1999;	99MO-US30911.
PR	20-DEC-1999;	99MO-US30999.
PR	22-DEC-1999;	99MO-US30720.
PR	22-DEC-1999;	99MO-US31243.
PR	30-DEC-1999;	99MO-US31274.
PR	05-JAN-2000;	2000MO-US00219.
PR	06-JAN-2000;	2000MO-US00277.
PR	11-FEB-2000;	2000MO-US00376.
PR	11-FEB-2000;	2000MO-US00355.
PR	18-FEB-2000;	2000MO-US04341.
PR	18-FEB-2000;	2000MO-US04342.
PR	22-FEB-2000;	2000MO-US04414.
PR	24-FEB-2000;	2000MO-US04914.
PR	24-FEB-2000;	2000MO-US05004.
PR	01-MAR-2000;	2000MO-US05601.
PR	02-MAR-2000;	2000MO-US05746.
PR	02-MAR-2000;	2000MO-US05681.
PR	10-MAR-2000;	2000MO-US06319.
PR	15-MAR-2000;	2000MO-US06884.
PR	20-MAR-2000;	2000MO-US07377.
PR	21-MAR-2000;	2000MO-US07532.
PR	30-MAR-2000;	2000MO-US06439.
PR	17-MAY-2000;	2000MO-US13705.
PR	22-MAY-2000;	2000MO-US14042.
PR	30-MAY-2000;	2000MO-US14941.
PR	02-JUN-2000;	2000MO-US20710.
PR	28-JUN-2000;	2000MO-US20710.
PR	11-AUG-2000;	2000MO-US22031.
PR	23-AUG-2000;	2000MO-US23522.
PR	24-AUG-2000;	2000MO-US23326.
PR	08-NOV-2000;	2000MO-US30952.
PR	10-NOV-2000;	2000MO-US30873.
PR	01-DEC-2000;	2000MO-US32678.
PR	20-DEC-2000;	2000MO-US34956.
PR	28-FEB-2001;	2001MO-US06520.
PR	01-MAR-2001;	2001MO-US06666.
PR	25-MAY-2001;	2001MO-US17092.
PR	01-JUN-2001;	2001MO-US17800.
PR	20-JUN-2001;	2001MO-US19692.
PR	22-JUN-2001;	2001MO-US20116.
PR	29-JUN-2001;	2001MO-US21735.
PR	30-DEC-2000;	2000MO-US74759.
PR	28-FEB-2001;	2001MO-US79648.
PR	09-MAR-2001;	2001MO-US80276.
PR	14-MAR-2001;	2001MO-US80569.
PR	22-MAR-2001;	2001MO-US81574.
PR	05-APR-2001;	2001MO-US82366.
PR	10-MAY-2001;	2001MO-US85428.
PR	10-MAY-2001;	2001MO-US85428.
PR	18-MAY-2001;	2001MO-US86012.
PR	25-MAY-2001;	2001MO-US86028.
PR	01-JUN-2001;	2001MO-US86034.
PR	01-JUN-2001;	2001MO-US87203.
PR	05-JUN-2001;	2001MO-US87453.
PR	14-JUN-2001;	2001MO-US88263.
PR	19-JUN-2001;	2001MO-US88634.
PR	21-JUN-2001;	2001MO-US88789.
PR	18-JUL-2001;	2001MO-US90882.
PR	06-AUG-2001;	2001MO-US92449.
PR	09-AUG-2001;	2001MO-US92796.
PR	16-AUG-2001;	2001MO-US93180.
PR	19-DEC-2001;	2001MO-US93872.

PI Smith V, Stewart TA, Tunas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-331925/31.
XX DR N-PSDB; ACA04224.
XX
XX
XX New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX
XX Claim 12; Fig 402; 659pp; English.
PS

cardiac insufficiency disorder; cancer; tumour; immune response;
adrenal cortical capillary endothelial growth; c-fos induction;
vascular endothelial growth factor inhibition; VEGF inhibition;
endothelial cell growth inhibitor; T-lymphocytes stimulation;
retinal neurons cell survival; rod photoreceptor cell survival;
retinal disorder; retinitis pigmentosa; kidney disorder;
mammalian kidney mesangial cell proliferation; Berger disease;
dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
chondrocyte redifferentiation; sports injury; arthritis.
Homo sapiens.
US2003017563-A1.
23-JAN-2003.
07-MAY-2002; 2002US-0140808.
31-MAR-1997; 97WO-US05230.
12-JUN-1998; 98WO-US12456.
14-JUL-1998; 98WO-US14552.
28-AUG-1998; 98WO-US17888.
10-SEP-1998; 98WO-US18824.
14-SEP-1998; 98WO-US19093.
14-SEP-1998; 98WO-US19094.
14-SEP-1998; 98WO-US19177.
16-SEP-1998; 98WO-US19330.
17-SEP-1998; 98WO-US19437.
29-OCT-1998; 98WO-US21141.
29-OCT-1998; 98WO-US22991.
29-OCT-1998; 98WO-US22992.
20-NOV-1998; 98WO-US24855.
01-DEC-1998; 98WO-US25108.
05-JAN-1999; 99WO-US00106.
08-MAR-1999; 99WO-US05028.
10-MAR-1999; 99WO-US05130.
20-APR-1999; 99WO-US08615.
14-MAY-1999; 99WO-US10733.
02-JUN-1999; 99WO-US12252.
01-SEP-1999; 99WO-US20111.
08-SEP-1999; 99WO-US20594.
13-SEP-1999; 99WO-US20944.
15-SEP-1999; 99WO-US21090.
15-SEP-1999; 99WO-US21547.
05-OCT-1999; 99WO-US23089.
29-NOV-1999; 99WO-US28214.
30-NOV-1999; 99WO-US28313.
30-NOV-1999; 99WO-US28409.
01-DEC-1999; 99WO-US28301.
01-DEC-1999; 99WO-US28634.
02-DEC-1999; 99WO-US28551.
02-DEC-1999; 99WO-US28564.
02-DEC-1999; 99WO-US28565.
16-DEC-1999; 99WO-US30095.
20-DEC-1999; 99WO-US30911.
20-DEC-1999; 99WO-US30999.
22-DEC-1999; 99WO-US30720.
30-DEC-1999; 99WO-US31243.
30-DEC-1999; 99WO-US31274.
05-JAN-2000; 2000WO-US00219.
06-JAN-2000; 2000WO-US00277.
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
24-FEB-2000; 2000WO-US04914.
24-FEB-2000; 2000WO-US05004.
01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05746.
02-MAR-2000; 2000WO-US05841.
10-MAR-2000; 2000WO-US06319.
15-MAR-2000; 2000WO-US06884.

20-MAR-2000; 2000WO-US07377.
21-MAR-2000; 2000WO-US07532.
30-MAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
28-JUL-2000; 2000WO-US20710.
11-AUG-2000; 2000WO-US22031.
23-AUG-2000; 2000WO-US23522.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
10-NOV-2000; 2000WO-US30873.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-MAR-2001; 2001WO-US06666.
25-MAY-2001; 2001WO-US17092.
01-JUN-2001; 2001WO-US17800.
20-JUN-2001; 2001WO-US19692.
22-JUN-2001; 2001WO-US20116.
29-JUN-2001; 2001WO-US21066.
09-JUL-2001; 2001WO-US21735.
28-FEB-2001; 2001US-0747259.
28-FEB-2001; 2001US-0796498.
09-MAR-2001; 2001US-0802706.
14-MAR-2001; 2001US-0809689.
22-MAR-2001; 2001US-0818744.
03-APR-2001; 2001US-0828366.
10-MAY-2001; 2001US-0854208.
18-MAY-2001; 2001US-0860216.
25-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
01-JUN-2001; 2001US-0872035.
05-JUN-2001; 2001US-0874503.
14-JUN-2001; 2001US-0882636.
19-JUN-2001; 2001US-0886342.
21-JUN-2001; 2001US-0887879.
18-JUL-2001; 2001US-0908827.
06-AUG-2001; 2001US-0924419.
09-AUG-2001; 2001US-0927796.
16-AUG-2001; 2001US-0931836.
19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;

WPI; 2003-148238/14.
N-PSDB; ABX89341.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
are therapeutically useful for enhancing immune response and in cancer
treatments .

Claim 12; Fig 402; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO
polypeptides are useful in detecting PRO polypeptides in a sample, in
linking a bioactive molecule to a cell expressing a PRO polypeptide, and
in modulating at least one biological activity of a cell expressing a PRO
polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
stimulate adrenal cortical capillary endothelial growth, and PRO536,
PRO943, PRO826, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
PRO1340 and PRO1387 induce c-fos in endothelial cells, and are thus
useful for treating conditions or disorders where angiogenesis would be
beneficial, e.g. wound healing and antagonist of this polypeptide are
useful for treating cancerous tumours. PRO812 inhibits vascular

endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO829, PRO826, PRO1068 or PRO1332 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.

XX Sequence 123 AA;

Query Match: 100.0%; Score 657; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MACRCLSPFLMGTFLVSQCTVLAQLDALLVPPGVAQLSCTLSPQHVTIRDYGVSWYQQR 60
Db 1 MACRCLSPFLMGTFLVSQCTVLAQLDALLVPPGVAQLSCTLSPQHVTIRDYGVSWYQQR 60
QY 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLITISVPQEDDADYCVGVG 120
Db 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLITISVPQEDDADYCVGVG 120
QY 121 FSP 123
Db 121 FSP 123

RESULT 9

ABUS9071
ID ABUS9071 standard; Protein; 123 AA.

XX AC ABUS9071;

XX DT 28-APR-2003 (first entry)

XX DE Novel human secreted or transmembrane protein PRO619.

XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
XX KW cardiac insufficiency disorder; cancer; tumour; immune response;
XX KW adrenal cortical capillary endothelial growth; c-fos induction;
XX KW vascular endothelial growth factor inhibition; VEGF inhibition;
XX KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
XX KW retinal neurons cell survival; rod photoreceptor cell survival;
XX KW retinal disorder; retinitis pigmentosa; kidney disease;
XX KW mammalian kidney mesangial cell proliferation; Berger disease;
XX KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX KW chondrocyte redifferentiation; sports injury; arthritis.

XX OS Homo sapiens.

XX PN US2002132252-A1.

XX PD 19-SEP-2002.

XX PF 14-NOV-2001; 2001US-0990442.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 16-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US00376.
PR 06-JAN-2000; 2000WO-US03565.
PR 11-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04414.
PR 22-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 24-FEB-2000; 2000WO-US05841.
PR 02-MAR-2000; 2000WO-US06319.
PR 10-MAR-2000; 2000WO-US06884.
PR 15-MAR-2000; 2000WO-US07377.
PR 20-MAR-2000; 2000WO-US08439.
PR 30-MAR-2000; 2000WO-US13358.
PR 15-MAY-2000; 2000WO-US13705.
PR 17-MAY-2000; 2000WO-US14042.
PR 22-MAY-2000; 2000WO-US14941.
PR 30-MAY-2000; 2000WO-US15264.
PR 02-JUN-2000; 2000WO-US20710.
PR 28-JUL-2000; 2000WO-US22031.
PR 11-AUG-2000; 2000WO-US23522.
PR 23-AUG-2000; 2000WO-US23328.
PR 24-AUG-2000; 2000WO-US23052.
PR 08-NOV-2000; 2000WO-US32878.
PR 01-DEC-2000; 2000WO-US32878.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062250P.
PR 12-NOV-1997; 97US-065186P.
PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087108P.
PR 02-JUN-1998; 98US-087607P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087599P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088021P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088030P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088655P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088734P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088742P.
PR 10-JUN-1998; 98US-088810P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088858P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089105P.

16-JUN-1998; 98US-089440P.
16-JUN-1998; 98US-089512P.
16-JUN-1998; 98US-089514P.
17-JUN-1998; 98US-089532P.
17-JUN-1998; 98US-089538P.
17-JUN-1998; 98US-089598P.
17-JUN-1998; 98US-089599P.
17-JUN-1998; 98US-089600P.
17-JUN-1998; 98US-089653P.
18-JUN-1998; 98US-089801P.
18-JUN-1998; 98US-089907P.
18-JUN-1998; 98US-089908P.
28-AUG-2001; 2001US-0941992.
(GETH) GENENTECH INC.
Askenazi AJ, Baker KP, Botstein D, Deanovs L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;
WPI; 2003-247083/24.
N-PSDB; ABX80195.
Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
are therapeutically useful for enhancing immune response and in cancer
treatments -
Claim 12; Fig 68; 648pp; English.
The invention describes an isolated human PRO polypeptide. The PRO
polypeptides are useful in detecting PRO polypeptides in a sample, in
linking a bioactive molecule to a cell expressing a PRO polypeptide, and
in modulating at least one biological activity of a cell expressing a PRO
polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
stimulate adrenal cortical capillary endothelial growth, and PRO536,
PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
useful for treating conditions or disorders where angiogenesis would be
beneficial, e.g. wound healing and antagonist of this polypeptide are
useful for treating cancerous tumours. PRO812 inhibits vascular
endothelial growth factor (VEGF) stimulated proliferation of endothelial
cells and is thus useful for inhibiting endothelial cell growth in
mammals which would be beneficial in inhibiting tumour growth. PRO826,
PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
stimulated T-lymphocytes and are therapeutically useful for enhancing
immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
retinal neurons cells (PRO1132 is also enhances survival/proliferation of
rod photoreceptor cells) and therefore are useful for treating retinal
disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
and PRO1066 induce proliferation of mammalian kidney mesangial cells,
and therefore are useful for treating kidney disorders associated with
decreased mesangial cell function such as Berger disease or Crohn's
nephropathies associated with dermatitis, herpeticiformis or Crohn's
disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
proliferation and/or redifferentiation of chondrocytes in culture and
are thus useful for treating sports injuries, and arthritis. This
is the amino acid sequence of a novel human PRO protein.

2y 1 MACCLSLMGTLSVQTVAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSNYQQR 60
db 1 MACCLSLMGTLSVQTVAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSNYQQR 60
2y 61 AGSAPRYLLYSEEDHRRPADIPDRFSAAKDEAHNACVLITISPVQPEDDADYICSVGYG 120

Db 61 AGSAPRYLLYSEEDHRRPADIPDRFSAAKDEAHNACVLITISPVQPEDDADYICSVGYG 120
Qy 121 FSP 123
Db 121 FSP 123
RESULT 10
ABUS9218
ID ABUS9218 standard; Protein; 123 AA.
XX AC ABUS9218;
XX DT 22-APR-2003 (first entry)
XX DE Human secreted/transmembrane protein, #43.
XX KW Human; PRO; secreted; transmembrane; pharmaceutical;
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.
XX OS Homo sapiens.
XX PN US2003027162-A1.
XX PD 06-FEB-2003.
XX PF 15-NOV-2001; 2001US-0997428.
XX PR 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 07-SEP-1998; 98WO-US19437.
PR 01-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12552.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.

PR	09-JUL-2001,	2001WO-US21735,
PR	16-JUN-1997,	97US-0437870P,
PR	17-OCT-1997,	97US-0622501P,
PR	12-NOV-1997,	97US-0651811P,
PR	13-NOV-1997,	97US-0653111P,
PR	24-FEB-1998,	97US-0667700P,
PR	25-FEB-1998,	97US-0759450P,
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PR	28-APR-1998,	98US-0833222P,
PR	07-MAY-1998,	98US-0846000P,
PR	28-MAY-1998,	98US-0871065P,
PR	02-JUN-1998,	98US-0876070P,
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PR	05-JUN-1998,	98US-0881617P,
PR	05-JUN-1998,	98US-0882023P,
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PR	05-JUN-1998,	98US-0882117P,
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PR	10-JUN-1998,	98US-0887343P,
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PR	10-JUN-1998,	98US-0887842P,
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PR	11-JUN-1998,	98US-0888651P,
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PR	12-JUN-1998,	98US-0891103P,
PR	16-JUN-1998,	98US-0894400P,
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PR	16-JUN-1998,	98US-0895114P,
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PR	17-JUN-1998,	98US-0895939P,
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PR	19-JUN-1998,	98US-0899452P,
PR	22-JUN-1998,	98US-0899252P,
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PR	23-JUN-1998,	98US-0903450P,
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PR	24-JUN-1998,	98US-0904445P,
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PR	24-JUN-1998,	98US-0905575P,
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PR	25-JUN-1998,	98US-0906949P,
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PR	25-JUN-1988	98US-0906962P
PR	26-JUN-1988	98US-0906862P
PR	26-JUN-1988	98US-0908663P
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PR	02-JUL-1988	98US-0914478P
PR	02-JUL-1988	98US-0915151P
PR	02-JUL-1988	98US-0916262P
PR	02-JUL-1988	98US-0916288P
PR	02-JUL-1988	98US-0916333P
PR	02-JUL-1988	98US-0916468P
PR	02-JUL-1988	98US-0916763P
PR	07-JUL-1988	98US-0919378P
PR	07-JUL-1988	98US-0919882P
PR	09-JUL-1988	98US-0921802P
PR	10-JUL-1988	98US-0924472P
PR	20-JUL-1988	98US-0933393P
PR	30-JUL-1988	98US-0945531P
PR	04-AUG-1988	98US-0952852P
PR	04-AUG-1988	98US-0952855P
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PR	04-AUG-1988	98US-0953028P
PR	04-AUG-1988	98US-0953121P
PR	04-AUG-1988	98US-0953255P
PR	10-AUG-1988	98US-0955163P
PR	10-AUG-1988	98US-0955293P
PR	10-AUG-1988	98US-096012P
PR	11-AUG-1988	98US-0961343P
PR	11-AUG-1988	98US-0961468P
PR	12-AUG-1988	98US-0962939P
PR	17-AUG-1988	98US-0967577P
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PR	17-AUG-1988	98US-0967733P
PR	17-AUG-1988	98US-0967919P
PR	17-AUG-1988	98US-0968677P
PR	17-AUG-1988	98US-0968911P
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PR	17-AUG-1988	98US-0968959P
PR	17-AUG-1988	98US-0968977P
PR	18-AUG-1988	98US-096949P
PR	18-AUG-1988	98US-0969509P
PR	18-AUG-1988	98US-0969606P
PR	18-AUG-1988	98US-0970022P
PR	19-AUG-1988	98US-0971411P
PR	20-AUG-1988	98US-0972188P
PR	24-AUG-1988	98US-0976613P
PR	24-AUG-1988	98US-0979522P
PR	26-AUG-1988	98US-0873543P
PR	26-AUG-1988	98US-0973553P
PR	26-AUG-1988	98US-0973711P
PR	26-AUG-1988	98US-0973748P
PR	26-AUG-1988	98US-0973788P
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PR	26-AUG-1988	98US-0973863P
PR	31-AUG-1988	98US-0980114P
PR	31-AUG-1988	98US-0982252P
PR	16-SEP-1988	98US-1006344P
PR	17-SEP-1988	98US-1008588P
PR	22-DEC-1988	98US-113296P
PR	12-MAR-1999	99US-1239577P
PR	23-JUN-1999	99US-1410377P

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100.0%; Score 657; DB 24; Length 123;

Query Match	100.0%;	score 937;	DB 274
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0v 1 MACRCLSELLMGTFELSVSOTVLAQLDALLVFFGOVAQLSCTLSPQHVTIRDYGVSWYQQR 60

1 MACRCISFELIMGTELSVSOTVLAOLDALLVFFGOVAOLSCISPOHVTIRDYGVSWYQQR 60

Y 61 AGSAPRYLLYRSEEDHHRPADIPORFSAKDEAHNACVLITSPVQPEDDADYYCYSVGYG 120
 b 61 AGSAPRYLLYRSEEDHHRPADIPORFSAKDEAHNACVLITSPVQPEDDADYYCYSVGYG 120
 Y 121 FSP 123
 b 121 FSP 123

ESULT 11
 BUE59367
 D AEU59367 standard; Protein; 123 AA.
 X C AEU59367;
 X T 22-APR-2003 (first entry)

Novel human secreted or transmembrane protein PRO943.
 Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 cardiac insufficiency disorder; cancer; tumour; immune response;
 adrenal cortical capillary endothelial growth; c-fos induction;
 vascular endothelial growth factor inhibition; VEGF inhibition;
 endothelial cell growth inhibitor; T-lymphocytes stimulation;
 retinal neurons cell survival; rod photoreceptor cell survival;
 retinal disorder; retinitis pigmentosa; kidney disorder;
 mammalian kidney mesangial cell proliferation; Berger disease;
 dermatitis; herpiformis; Crohn's disease; chondrocyte proliferation;
 chondrocyte redifferentiation; sports injury; arthritis.

Homo sapiens.
 US2003027985-A1.
 06-FEB-2003.

14-NOV-2001; 2001US-0990562.
 05-NOV-1997; 97WO-US200069.
 16-SEP-1998; 98WO-US19330.
 17-SEP-1998; 98WO-US19437.
 07-OCT-1998; 98WO-US21141.
 01-DEC-1998; 98WO-US25108.
 05-JAN-1999; 99WO-US00106.
 08-MAR-1999; 99WO-US05028.
 02-JUN-1999; 99WO-US12252.
 15-SEP-1999; 99WO-US21090.
 15-SEP-1999; 99WO-US21547.
 30-NOV-1999; 99WO-US28313.
 01-DEC-1999; 99WO-US28301.
 01-DEC-1999; 99WO-US28634.
 16-DEC-1999; 99WO-US30095.
 20-DEC-1999; 99WO-US30911.
 05-JAN-2000; 2000WO-US00219.
 06-JAN-2000; 2000WO-US00376.
 11-FEB-2000; 2000WO-US03565.
 18-FEB-2000; 2000WO-US04341.
 22-FEB-2000; 2000WO-US04414.
 24-FEB-2000; 2000WO-US04914.
 24-FEB-2000; 2000WO-US05004.
 02-MAR-2000; 2000WO-US05841.
 10-MAR-2000; 2000WO-US06319.
 15-MAR-2000; 2000WO-US06884.
 20-MAR-2000; 2000WO-US07377.
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 17-MAY-2000; 2000WO-US13705.
 22-MAY-2000; 2000WO-US14042.
 30-MAY-2000; 2000WO-US14941.
 02-JUN-2000; 2000WO-US15264.
 28-JUL-2000; 2000WO-US20710.
 11-AUG-2000; 2000WO-US22031.
 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.
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 PR 11-JUN-1998; 98US-088861P.
 PR 11-JUN-1998; 98US-088876P.
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 PR 17-JUN-1998; 98US-089653P.
 PR 18-JUN-1998; 98US-089801P.
 PR 18-JUN-1998; 98US-089807P.
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 PR 19-JUN-1998; 98US-089947P.
 PR 19-JUN-1998; 98US-089948P.
 PR 19-JUN-1998; 98US-089952P.
 PR 22-JUN-1998; 98US-090246P.
 PR 22-JUN-1998; 98US-090252P.
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 PR 24-JUN-1998; 98US-090431P.
 PR 24-JUN-1998; 98US-090435P.
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 PR 24-JUN-1998; 98US-090445P.
 PR 24-JUN-1998; 98US-090472P.
 PR 24-JUN-1998; 98US-090535P.
 PR 24-JUN-1998; 98US-090540P.

PR 24-JUN-1998; 98US-090542P.
PR 24-JUN-1998; 98US-090557P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 01-JUL-1998; 98US-091360P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091519P.
PR 02-JUL-1998; 98US-091626P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091633P.
PR 02-JUL-1998; 98US-091646P.
PR 02-JUL-1998; 98US-091673P.
PR 07-JUL-1998; 98US-091978P.
PR 07-JUL-1998; 98US-091982P.
PR 09-JUL-1998; 98US-092182P.
PR 10-JUL-1998; 98US-092472P.
PR 20-JUL-1998; 98US-093339P.
PR 30-JUL-1998; 98US-094851P.
PR 04-AUG-1998; 98US-095282P.
PR 04-AUG-1998; 98US-095285P.
PR 04-AUG-1998; 98US-095301P.
PR 04-AUG-1998; 98US-095302P.
PR 04-AUG-1998; 98US-095318P.
PR 04-AUG-1998; 98US-095321P.
PR 04-AUG-1998; 98US-095325P.
PR 10-AUG-1998; 98US-095916P.
PR 10-AUG-1998; 98US-095929P.
PR 10-AUG-1998; 98US-096012P.
PR 11-AUG-1998; 98US-096143P.
PR 11-AUG-1998; 98US-096146P.
PR 12-AUG-1998; 98US-096329P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096773P.
PR 17-AUG-1998; 98US-096791P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096894P.
PR 17-AUG-1998; 98US-096895P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096950P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-096960P.
PR 18-AUG-1998; 98US-097022P.
PR 19-AUG-1998; 98US-097141P.
PR 20-AUG-1998; 98US-097218P.
PR 24-AUG-1998; 98US-097661P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-097978P.
PR 26-AUG-1998; 98US-097979P.
PR 26-AUG-1998; 98US-097986P.
PR 26-AUG-1998; 98US-098014P.

Query Match 100.0%; Score 657; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MACRCISFLIMGTFLSVSQTVLIAQLDALLVFPFGVAQLSCTLSPOHVTIRDYGVSWYQQR 60
1 MACRCISFLIMGTFLSVSQTVLIAQLDALLVFPFGVAQLSCTLSPOHVTIRDYGVSWYQQR 60

Qy 61 AGSAPYLLYRSEEDHHPADIPDRFSAKDEAHNACVLITISVPQEDDADYYCSGVG 120
Db 61 AGSAPYLLYRSEEDHHPADIPDRFSAKDEAHNACVLITISVPQEDDADYYCSGVG 120
Qy 121 FSP 123
Db 121 FSP 123
RESULT 12
ABU60502
ID ABU60502 standard; Protein; 123 AA.
XX
AC ABU60502;
XX
XX 01-MAY-2003 (first entry)
XX Human secreted/transmembrane protein, #43.
DE Human; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; therapeutic; gene therapy.
KW
OS Homo sapiens.
XX
XX US2002160384-A1.
XX
XX 31-OCT-2002.
XX
XX 14-NOV-2001; 2001US-0992598.
XX
XX 05-NOV-1997; 97WO-US200069.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 07-OCT-1998; 98WO-US21141.
XX 01-DEC-1998; 98WO-US25108.
XX 05-JAN-1999; 99WO-US00106.
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12552.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28301.
XX 16-DEC-1999; 99WO-US28634.
XX 20-DEC-1999; 99WO-US30095.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03585.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 02-MAR-2000; 2000WO-US05841.
XX 10-MAR-2000; 2000WO-US06319.
XX 15-MAR-2000; 2000WO-US06884.
XX 20-MAR-2000; 2000WO-US07377.
XX 30-MAR-2000; 2000WO-US08439.
XX 15-MAY-2000; 2000WO-US13358.
XX 17-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US15284.
XX 28-JUL-2000; 2000WO-US20710.
XX 11-AUG-2000; 2000WO-US22031.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 08-NOV-2000; 2000WO-US30952.
XX 01-DEC-2000; 2000WO-US32678.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-JUN-2001; 2001WO-US17800.
XX 20-JUN-2001; 2001WO-US19692.
XX 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062250P.
PR 12-NOV-1997; 97US-065186P.
PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
PR 02-JUN-1998; 98US-087607P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088021P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088026P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088030P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088734P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088742P.
PR 10-JUN-1998; 98US-088810P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088858P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089440P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089532P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089599P.
PR 17-JUN-1998; 98US-089600P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089801P.
PR 18-JUN-1998; 98US-089907P.
PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-0941992.

(GETH) GENENTECH INC.

PR Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PR Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PR Grimaldi JC, Gurney AL, Klijavin IJ, Napier MA, Pan J, Paoni NF,
PR Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PR Zhang Z;

XX WPI; 2003-288106/28.
XX N-PSDB; ABX90174.

XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
FT chromosome markers, or in generating probes -

XX Claim 12; Fig 68; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive

CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein
CC electrophoresis, and the isolated nucleic acids may be used for
CC recombinantly expressing those markers. The PRO polypeptides and nucleic
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful
CC in diagnostic assays for PRO, and in affinity purification of PRO from
CC recombinant cell culture or natural sources. The sequences presented in
CC ABU60478-ABU60624 are the PRO polynucleotides of the invention.
CC Note: The sequence data for this patent is also available in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 123 AA;

Query Match 100.0%; Score 657; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. NO. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRCLSFLIMGTFLSVSQTIVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60
Db 1 MACRCLSFLIMGTFLSVSQTIVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60
QY 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYICSVGYG 120
Db 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYICSVGYG 120
QY 121 FSP 123
Db 121 FSP 123

RESULT 13

ABU57993
ID ABU57993 standard; Protein; 123 AA.

XX AC ABU57993;

XX DT 14-APR-2003 (first entry)

XX DE Human PRO polypeptide #25.

XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
XX antibody-dependent enzyme mediated prodrug therapy.

XX OS Homo sapiens.

XX PN US2003027163-A1.

XX PD 06-FEB-2003.

XX PF 15-NOV-2001; 2001US-0997666.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 01-DEC-1999; 99WO-US28634.

XX PR 16-DEC-1999; 99WO-US30095.

XX PR 20-DEC-1999; 99WO-US30911.

XX PR 05-JAN-2000; 2000WO-US00219.

XX PR 06-JAN-2000; 2000WO-US00376.

XX PR 11-FEB-2000; 2000WO-US03565.


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R 26-AUG-1998; 98US-097952P.
R 26-AUG-1998; 98US-097954P.
R 26-AUG-1998; 98US-097955P.
R 26-AUG-1998; 98US-097971P.
R 26-AUG-1998; 98US-097974P.
R 26-AUG-1998; 98US-097978P.
R 26-AUG-1998; 98US-097979P.
R 26-AUG-1998; 98US-097986P.
R 26-AUG-1998; 98US-098014P.
R 31-AUG-1998; 98US-098525P.
R 16-SEP-1998; 98US-100634P.
R 17-SEP-1998; 98US-100858P.
R 22-DEC-1998; 98US-113296P.
R 12-MAR-1999; 98US-123957P.
R 23-JUN-1999; 98US-141037P.
R 07-JUL-1999; 98US-143048P.

Query Match 100.0%; Score 657; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 5,9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MACRCLFLLMGTFLSVQTFLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
b 1 MACRCLFLLMGTFLSVQTFLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60

Y 61 AGAPRYLLYRSEEDHRRPADIPDRFSAKDAAHNAACVLTITSPQPEDDADYYCSVGYG 120
b 61 AGAPRYLLYRSEEDHRRPADIPDRFSAKDAAHNAACVLTITSPQPEDDADYYCSVGYG 120

Y 121 FSP 123
b 121 FSP 123

RESULT 14
ABUS8924
D ABUS8924 standard; Protein; 123 AA.
C ABUS8924;
X 16-APR-2003 (first entry)
X Human secreted/transmembrane protein, #43.
X Human; PRO; secreted; transmembrane; signal peptide;
X pharmaceutical; diagnostic; biosensor; tumour; therapeutic;
X colon cancer; lung cancer; breast cancer; cancer; gene therapy.
X Homo sapiens.
X US2002142961-A1.
X 03-OCT-2002.
X 19-NOV-2001; 2001US-0989721.
X 05-NOV-1997; 97WO-US20069.
X 17-SEP-1998; 98WO-US19437.
X 07-OCT-1998; 98WO-US21141.
X 01-DEC-1998; 98WO-US25108.
X 05-JAN-1999; 99WO-US00106.
X 08-MAR-1999; 99WO-US05028.
X 02-JUN-1999; 99WO-US12252.
X 15-SEP-1999; 99WO-US21090.
X 30-NOV-1999; 99WO-US21547.
X 01-DEC-1999; 99WO-US28313.
X 01-DEC-1999; 99WO-US28301.
X 01-DEC-1999; 99WO-US28634.
X 16-DEC-1999; 99WO-US30095.
X 20-DEC-1999; 99WO-US30911.
X 05-JAN-2000; 2000WO-US00219.
X 06-JAN-2000; 2000WO-US00376.
X 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062250P.
PR 12-NOV-1997; 97US-065186P.
PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075345P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
PR 02-JUN-1998; 98US-087607P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088021P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088026P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088030P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088555P.
PR 10-JUN-1998; 98US-088734P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088742P.
PR 10-JUN-1998; 98US-088810P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088858P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089440P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089532P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089599P.
PR 17-JUN-1998; 98US-089600P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089801P.
PR 18-JUN-1998; 98US-089907P.

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PR 18-JUN-1998; 98US-089908P.
XX 28-AUG-2001; 2001US-0941992.
XX (GETH) GENENTECH INC.
XX Askenazi AJ, Baker KP, Botstein D, Deanovers L, Eaton DL;
PI Ferrarini N, Fong S, Gerber H, Geritsein ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FW, Wood WI;
PI Zhang Z;
XX WPI; 2003-155950/15.
XX
XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,
PT PRO361 or PRO846) useful as targets for therapeutic intervention in
PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers
PT
XX
XX Claim 12; Fig 68; 647pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors, for detecting or treating e.g. tumours in
CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, goats or
CC rabbits as targets for therapeutic intervention in certain cancers (e.g.
CC colon, lung or breast cancers) and diagnostic determination of the
CC presence of these cancers. The PRO polypeptides are also useful as
CC molecular weight markers or for chromosome identification. The PRO genes
CC are useful as hybridisation probes or for screening libraries of human
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The sequences
CC presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention.
XX
SQ Sequence 123 AA;
Query Match 100.0%; Score 657; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MACRCLSFLLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSMTQQR 60
Db |||||
1 MACRCLSFLLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSMTQQR 60
QY 61 AGSAPRYLLYRSEEDHHRPADIPRFSAAKDEAHNACVLTISVPQEDDADYCSVGYG 120
Db |||||
61 AGSAPRYLLYRSEEDHHRPADIPRFSAAKDEAHNACVLTISVPQEDDADYCSVGYG 120
QY 121 FSP 123
Db |||||
121 FSP 123
RESULT 15
ABU1384
ID ABU1384 standard; Protein; 123 AA.
XX
XX ABU1384;
AC
XX
XX 26-FEB-2003 (first entry)
DT
XX Human PRO619 polypeptide.
DE
XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW Genetic disorder; antibacterial; immunosuppressive.
KW
XX Homo sapiens.
OS
XX US2002103125-A1.
PN

XX 01-AUG-2002.
XX 20-NOV-2001; 2001US-0989731.
XX
XX 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 16-DEC-1999; 99WO-US30911.
PR 06-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04514.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US15264.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-045787P.
PR 17-OCT-1997; 97US-062250P.
PR 12-NOV-1997; 97US-065186P.
PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
PR 02-JUN-1998; 98US-087607P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-088021P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088026P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088030P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.

PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088734P.
PR 10-JUN-1998; 98US-088738P.
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PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089440P.
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PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089532P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089599P.
PR 17-JUN-1998; 98US-089600P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089801P.
PR 18-JUN-1998; 98US-089907P.
PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-094199Z.
XX
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(GETH) GENENTECH LTD.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Pacini NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX

DR WPI; 2003-102117/09.
DR N-PSDB; ABX64020.
XX

PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers -
XX

PS Claim 12; Fig 68; 649pp; English.
XX

CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, to construct
CC hybridisation probes for mapping the gene which encodes the PRO
CC polypeptide, and for the genetic analysis of individuals with genetic
CC disorders, in gene therapy, for chromosome identification, as
CC chromosome markers, and for generating probes for PCR, Northern
CC analysis, Southern analysis and Western analysis. ABU13860-ABU14006
CC represent the human PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipidentry.html.
XX

SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MACRCLSLMGTFLSVSQTVLAQLDALLVFPQVLAQLSCTLSPOHVTIRDYGVSWYQOR 60
DB 1 MACRCLSLMGTFLSVSQTVLAQLDALLVFPQVLAQLSCTLSPOHVTIRDYGVSWYQOR 60

OY 61 AGSAPRYLLYTRSEEDHHRPADIPDRFSAKDRAHNAACVLTITSPVQPEDDADYICVGVG 120
Db 61 AGSAPRYLLYTRSEEDHHRPADIPDRFSAKDRAHNAACVLTITSPVQPEDDADYICVGVG 120
OY 121 FSP 123
Db 121 FSP 123

Search completed: February 9, 2004, 12:45:51
Job time : 41.2297 secs

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PRIOR APPLICATION NUMBER:	60/089514
PRIOR FILING DATE:	1998-06-16
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PRIOR APPLICATION NUMBER:	60/090863
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/090866
PRIOR FILING DATE:	1998-06-26

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; PRIOR APPLICATION NUMBER: 60/091360
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 657; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,1e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRLSFLMGTSLVSQTVLAQLDALLVFPQGVLAQLSCTLSPOHVTIRDYGVSWYQOR 60
DB 1 MACRLSFLMGTSLVSQTVLAQLDALLVFPQGVLAQLSCTLSPOHVTIRDYGVSWYQOR 60

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DB 61 AGSAPRYLLYRSDEHRRPADIPDRFSAAKDEAHNACVLITISFVQPEDADYVCSGVG 120

QY 121 FSP 123
DB 121 FSP 123

RESULT 2
JS-09-989-723-117
; Sequence 117, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 657; DB 9; Length 123;
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Db 121 FSP 123
RESULT 3
US-09-989-279-117
; Sequence 117, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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PRIOR APPLICATION NUMBER: 60/089512
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,1e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MACRCLSFLLMGTFLSVSTVLQDLALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
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RESULT 4

US-09-989-727-117
Sequence 117, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787

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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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DB 1 MACRCLSFLLMGTFLLSVSQTVLAQLDALLVFPQGVQVQLSCTLSFQVHTIRDYGVSWYQQR 60
QY 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISPQEDDADYYCSVGYG 120
DB 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISPQEDDADYYCSVGYG 120
QY 121 RSP 123
DB 121 RSP 123

RESULT 5
US-09-989-731-117
; Sequence 117, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20

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PRIOR FILING DATE: 1998-07-09

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JS-09-989-732-117
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Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Gerber, Hanspeter
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730F1C57
CURRENT APPLICATION NUMBER: US/09/989,732

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;; PRIOR FILING DATE: 1998-07-09
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Best Local Similarity 100.0%; Pred. No. 2.1e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MACRCISFLMGTFLLSVQTVLAQDLALLVFPQVAQLSCTLSPQHVTRDYGVSWYQOR 60
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QY 121 FSP 123
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RESULT 7
US-09-981-073-117
Sequence 117, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C15

CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,1e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRCLSLMGTFSLVSQTVLAQDALLVPGQVAGLSCTLSPOHVTIRDYGVSWYQOR 60
DB 1 MACRCLSLMGTFSLVSQTVLAQDALLVPGQVAGLSCTLSPOHVTIRDYGVSWYQOR 60

QY 61 AGSAPRYLLYRSEEDHRRPADIDRFSAAKDEAHNAACVLITISPVQFEDDADYICSVGYG 120
DB 61 AGSAPRYLLYRSEEDHRRPADIDRFSAAKDEAHNAACVLITISPVQFEDDADYICSVGYG 120

QY 121 FSP 123
DB 121 FSP 123

RESULT 8

US-09-990-442-117
Sequence 117, Application US/09990442
Patent No. US2002013225A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730PIC8
CURRENT APPLICATION NUMBER: US/09/990,442
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 PRIOR APPLICATION NUMBER: 60/090695

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 PRIOR FILING DATE: 1998-07-01
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 PRIOR FILING DATE: 1998-07-02
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;

Best Local Similarity 100.0%; Pred. No. 2.le-63; Indels 0; Gaps 0;
 Matches 123; Conservative 0; Mismatches 0;

QY 1 MACRCLSFLMGTFLSVSQTVLQAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
 DB 1 MACRCLSFLMGTFLSVSQTVLQAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
 QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYICSVGYG 120
 DB 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYICSVGYG 120
 QY 121 FSP 123
 DB 121 FSP 123

RESULT 9

US-09-991-163-117
 Sequence 117, Application US/09991163
 Patent No. US20020132253A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: KJavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,1e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 MACRLSFLMGTLVSQVTLAQDLALVPCQVAQLSCTLSPOHVTIRYGVSWYQOR 60
b 1 MACRLSFLMGTLVSQVTLAQDLALVPCQVAQLSCTLSPOHVTIRYGVSWYQOR 60

y 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYICSVGYG 120
b 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYICSVGYG 120

y 121 FSP 123
b 121 FSP 123

RESULT 10
IS-09-993-604-117
Sequence 117, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Gerritsen, Mary E.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-63; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0;

QY 1 MACRCLSFILMGTFILSVQTVLAQLDALLVFPQVQAQSCITLSPQHVITRDYGVSWYQQR 60
DB 1 MACRCLSFILMGTFILSVQTVLAQLDALLVFPQVQAQSCITLSPQHVITRDYGVSWYQQR 60

QY 61 AGSAPRYLLVYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPQPEDDADYICSVGYG 120
DB 61 AGSAPRYLLVYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPQPEDDADYICSVGYG 120

QY 121 FSP 123
DB 121 FSP 123

RESULT 11
US-09-990-456-117
Sequence 117, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,1e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 MACRCLSLFLMGTFLSVSTVLAQLDALLVFPQVAQLSCTLSPQHVTRIDYGVSWYQOR 60
b 1 MACRCLSLFLMGTFLSVSTVLAQLDALLVFPQVAQLSCTLSPQHVTRIDYGVSWYQOR 60
Y 61 AGAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNAVCVLTISPQVEDDADYCSVGYG 120
b 61 AGAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNAVCVLTISPQVEDDADYCSVGYG 120
Y 121 FSP 123
b 121 FSP 123

RESULT 12
JS-09-989-721-117
Sequence 117, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C55
CURRENT APPLICATION NUMBER: US/09/989,721
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090678
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PRIOR APPLICATION NUMBER: 60/090690

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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. Nc. 2.le-63; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0;

QY 1 MACRCISFLMGTFLLSVSQTVLALQDLALLVFPFGVAQLSCTLSPOHVTIRDYGVSWYQOR 60
DB 1 MACRCISFLMGTFLLSVSQTVLALQDLALLVFPFGVAQLSCTLSPOHVTIRDYGVSWYQOR 60

QY 61 AGSAPRYLLYRSEEDHHRPADIPRFSAAKDEAHNACVLTISPQPEDDADYCVSYG 120
DB 61 AGSAPRYLLYRSEEDHHRPADIPRFSAAKDEAHNACVLTISPQPEDDADYCVSYG 120

QY 121 FSP 123
DB 121 FSP 123

RESULT 13
US-09-992-598-117
Sequence 117, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C20
 CURRENT APPLICATION NUMBER: US/09/992,598
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

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RESULT 14
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 Patent No. US20020164669A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 70 Human Secreted Proteins
 FILE REFERENCE: P2001P1
 CURRENT APPLICATION NUMBER: US/09/981,876
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RESULT 15
US-09-989-293A-117
Sequence 117, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deanoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
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Best Local Similarity 100.0%; Pred. No. 2.1e-63;
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	201.5	30.7	249	4	US-08-918-148-79 Sequence 74, Appl
3	193	29.4	109	3	US-09-157-370-5 Sequence 5, Appl
4	193	29.4	245	4	US-10-039-785-42 Sequence 42, Appl
5	191	29.1	110	1	US-07-988-923-16 Sequence 16, Appl
6	191	29.1	110	2	US-08-362-780-16 Sequence 10, Appl
7	187	28.5	235	3	US-09-049-672A-10 Sequence 49, Appl
8	187	28.5	245	4	US-10-039-785-49 Sequence 6, Appl
9	186.5	28.4	238	4	US-08-793-450-6 Sequence 34, Appl
10	186	28.3	107	4	US-09-025-769B-34 Sequence 55, Appl
11	186	28.3	112	2	US-09-025-769B-55 Sequence 39, Appl
12	186	28.3	112	4	US-08-665-202-39 Sequence 39, Appl
13	186	28.3	112	4	US-09-315-574-39 Sequence 39, Appl
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15	183	27.9	109	4	US-09-025-769B-32 Sequence 32, Appl
16	183	27.9	109	4	US-09-025-769B-51 Sequence 51, Appl
17	183	27.9	111	2	US-08-652-816A-15 Sequence 48, Appl
18	183	27.9	245	4	US-10-039-785-48 Sequence 5, Appl
19	183	27.9	258	2	US-08-665-202-5 Sequence 5, Appl
20	183	27.9	258	4	US-09-315-574-5 Sequence 51, Appl
21	182	27.7	245	4	US-10-039-785-51 Sequence 52, Appl
22	182	27.7	245	4	US-10-039-785-52 Sequence 63, Appl
23	181.5	27.6	110	3	US-09-240-274-63 Sequence 14, Appl
24	181.5	27.6	111	2	US-08-958-201-14 Sequence 7, Appl
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280 3 US-09-260-527-1
234 4 US-09-372-425A-4
110 4 US-09-025-769B-33
110 4 US-09-025-769B-53
112 4 US-09-025-769B-19
113 1 US-08-211-202-112

ALIGNMENTS

RESULT 1
US-09-996-243-117
; Sequence 117, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fogt, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28

1	PRIOR FILING DATE: 1998-06-17	
2	PRIOR APPLICATION NUMBER: 60/089533	
3	PRIOR FILING DATE: 1998-06-17	
4	PRIOR APPLICATION NUMBER: 60/089801	
5	PRIOR FILING DATE: 1998-06-18	
6	PRIOR APPLICATION NUMBER: 60/089907	
7	PRIOR FILING DATE: 1998-06-18	
8	PRIOR APPLICATION NUMBER: 60/089908	
9	PRIOR FILING DATE: 1998-06-18	
10	PRIOR APPLICATION NUMBER: 60/089947	
11	PRIOR FILING DATE: 1998-06-19	
12	PRIOR APPLICATION NUMBER: 60/089948	
13	PRIOR FILING DATE: 1998-06-19	
14	PRIOR APPLICATION NUMBER: 60/089952	
15	PRIOR FILING DATE: 1998-06-19	
16	PRIOR APPLICATION NUMBER: 60/090246	
17	PRIOR FILING DATE: 1998-06-22	
18	PRIOR APPLICATION NUMBER: 60/090252	
19	PRIOR FILING DATE: 1998-06-22	
20	PRIOR APPLICATION NUMBER: 60/090254	
21	PRIOR FILING DATE: 1998-06-22	
22	PRIOR APPLICATION NUMBER: 60/090349	
23	PRIOR FILING DATE: 1998-06-23	
24	PRIOR APPLICATION NUMBER: 60/090355	
25	PRIOR FILING DATE: 1998-06-23	
26	PRIOR APPLICATION NUMBER: 60/090429	
27	PRIOR FILING DATE: 1998-06-24	
28	PRIOR APPLICATION NUMBER: 60/090431	
29	PRIOR FILING DATE: 1998-06-24	
30	PRIOR APPLICATION NUMBER: 60/090435	
31	PRIOR FILING DATE: 1998-06-24	
32	PRIOR APPLICATION NUMBER: 60/090444	
33	PRIOR FILING DATE: 1998-06-24	
34	PRIOR APPLICATION NUMBER: 60/090445	
35	PRIOR FILING DATE: 1998-06-24	
36	PRIOR APPLICATION NUMBER: 60/090472	
37	PRIOR FILING DATE: 1998-06-24	
38	PRIOR APPLICATION NUMBER: 60/090535	
39	PRIOR FILING DATE: 1998-06-24	
40	PRIOR APPLICATION NUMBER: 60/090540	
41	PRIOR FILING DATE: 1998-06-24	
42	PRIOR APPLICATION NUMBER: 60/090542	
43	PRIOR FILING DATE: 1998-06-24	
44	PRIOR APPLICATION NUMBER: 60/090557	
45	PRIOR FILING DATE: 1998-06-24	
46	PRIOR APPLICATION NUMBER: 60/090676	
47	PRIOR FILING DATE: 1998-06-25	
48	PRIOR APPLICATION NUMBER: 60/090678	
49	PRIOR FILING DATE: 1998-06-25	
50	PRIOR APPLICATION NUMBER: 60/090690	
51	PRIOR FILING DATE: 1998-06-25	
52	PRIOR APPLICATION NUMBER: 60/090694	
53	PRIOR FILING DATE: 1998-06-25	
54	PRIOR APPLICATION NUMBER: 60/090695	
55	PRIOR FILING DATE: 1998-06-25	
56	PRIOR APPLICATION NUMBER: 60/090696	
57	PRIOR FILING DATE: 1998-06-25	
58	PRIOR APPLICATION NUMBER: 60/090862	
59	PRIOR FILING DATE: 1998-06-26	
60	PRIOR APPLICATION NUMBER: 60/090863	
61	PRIOR FILING DATE: 1998-06-26	
62	PRIOR APPLICATION NUMBER: 60/091360	
63	PRIOR FILING DATE: 1998-07-01	
64	PRIOR APPLICATION NUMBER: 60/091478	
65	PRIOR FILING DATE: 1998-07-02	
66	PRIOR APPLICATION NUMBER: 60/091544	
67	PRIOR FILING DATE: 1998-07-01	
68	PRIOR APPLICATION NUMBER: 60/091519	
69	PRIOR FILING DATE: 1998-07-02	
70	PRIOR APPLICATION NUMBER: 60/091626	
71	PRIOR FILING DATE: 1998-07-02	
72	PRIOR APPLICATION NUMBER: 60/091633	
73	PRIOR FILING DATE: 1998-07-02	

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.6e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MACRCFLILMGTFILSVQTLAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSVYQOR 60
1 MACRCFLILMGTFILSVQTLAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSVYQOR 60

61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCSVG 120
61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCSVG 120

121 FSP 123
121 FSP 123

RESULT 2
S-08-918-148-74
Sequence 74, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 74
LENGTH: 249
TYPE: PRT
ORGANISM: artificial
S-08-918-148-74

Query Match 30.7%; Score 201.5; DB 4; Length 249;
Best Local Similarity 47.5%; Pred. No. 8.3e-14;
Matches 47; Conservative 16; Mismatches 29; Indels 7; Gaps 3;

18 SQTVAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSVYQORAGSAPRYLLYRSEEDH 77
136 SQSVLTQPASVSGSPQSITISCTGTSSGVGGYNY-VSWYQQHPGKAPKLLIYGN- 190

78 HRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCS 116
191 NRPSGVDRFSAK--SGNTASLTISGLQAEDEADYFCS 227

RESULT 3
S-09-157-370-5
Sequence 5, Application US/09157370A
Patent No. 626238
GENERAL INFORMATION:
APPLICANT: STEIPE, Boris
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P8341-8072
CURRENT APPLICATION NUMBER: US/09/157,370A
CURRENT FILING DATE: 1998-09-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER FILING DATE: 1997-01-14
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER FILING DATE: 1995-07-06

EARLIER APPLICATION NUMBER: DE/P44 25 115.7
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-157-370-5

Query Match 29.4%; Score 193; DB 3; Length 109;
Best Local Similarity 41.7%; Pred. No. 2.4e-13;
Matches 45; Conservative 18; Mismatches 29; Indels 16; Gaps 4;

QY 19 QTVLAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSVYQORAGSAPRYLLYRSEEDH 78
DB 1 QSELTQPPSVSPGQVTITSCGSDSLGIGY----VSWYQQHPGKAPKLLIY----DDNK 52

QY 79 RPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYC-----SVGYG 120
DB 53 RPSGIPDRFSGSK--SGNTASLTISGLQAEDEADYYCQSWDSSSVVFG 98

RESULT 4
US-10-039-785-42
Sequence 42, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 245
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: T1014A04 scFv
US-10-039-785-42

Query Match 29.4%; Score 193; DB 4; Length 245;
Best Local Similarity 38.5%; Pred. No. 6.5e-13;
Matches 47; Conservative 19; Mismatches 32; Indels 24; Gaps 4;

QY 12 GTFLSVS-----QTVLAQLDALLVPPGVAQLSCTLSPOHVTIRDYGV 54
DB 111 GTWVTVSSGGGGGGGGGSAQSVLTQPPSAGSPGQSVTISCTGTSDVGGYNY-V 169

QY 55 SWYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYY 114
DB 170 SWYQHPGKAPKLLIYGVNQ-----RPSGVDRFSGSK--SGNTASLTISGLQAEDEADYY 223

Y 115 CS 116
b 224 CS 225

RESULT 5
S-07-988-925-16
Sequence 16, Application US/07988925
Patent No. 5585097

GENERAL INFORMATION:
APPLICANT: Bolt, Sarah L.
APPLICANT: Clark, Michael R.
APPLICANT: Gorman, Scott D.
APPLICANT: Routledge, Edward G.
TITLE OF INVENTION: antibody preparation
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye pc
STREET: 11th Floor, 1100 No. 5985097th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,925
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: WO PCT/GB92/01933
FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-988-925-16

Query Match 29.1%; Score 191; DB 1; Length 110;
Best Local Similarity 43.2%; Pred. No. 4e-13;
Matches 41; Conservative 17; Mismatches 31; Indels 6; Gaps 2;

QY 21 VLAQDALIVFPQVAQLSCTLSPOHVTIRDYGVSWYQQAGSAPRYLLYRSEEDHHP 80
Db 3 MLTQPHSVSESFGKTVIISCTLSGN--IENNYVHWYQQRPGRAPTVIF----DDKRP 56

QY 81 ADIPDRFGSAKDEAHNACVLTISPQPEDDADYIC 115
Db 57 DGVPRFSGSIDRSSNSASLTISGLQTEDEADYIC 91

RESULT 6
US-08-362-780-16
Sequence 15, Application US/08362780
Patent No. 5968509
GENERAL INFORMATION:

APPLICANT: Gorman, Scott D.
APPLICANT: Routledge, Edward G.
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: Antibody Preparation
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye pc
STREET: 8th Floor, 1100 No. 5968509th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,780
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/962,543
FILING DATE: 23-JUNE-1992
APPLICATION NUMBER: GB 9021679.7
FILING DATE: 05-OCT-1990
APPLICATION NUMBER: WO PCT/GB91/01726
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-362-780-16

Query Match 29.1%; Score 191; DB 2; Length 110;
Best Local Similarity 43.2%; Pred. No. 4e-13;
Matches 41; Conservative 17; Mismatches 31; Indels 6; Gaps 2;

QY 21 VLAQDALIVFPQVAQLSCTLSPOHVTIRDYGVSWYQQAGSAPRYLLYRSEEDHHP 80
Db 3 MLTQPHSVSESFGKTVIISCTLSGN--IENNYVHWYQQRPGRAPTVIF----DDKRP 56

QY 81 ADIPDRFGSAKDEAHNACVLTISPQPEDDADYIC 115
Db 57 DGVPRFSGSIDRSSNSASLTISGLQTEDEADYIC 91

RESULT 7
US-09-049-672A-10
Sequence 10, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrione, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THYRN0T10
CLONE: 2872705
S-09-049-672A-10

Query Match 28.5%; Score 187; DB 3; Length 235;
Best Local Similarity 42.3%; Pred. No. 2.7e-12;
Matches 47; Conservative 20; Mismatches 36; Indels 8; Gaps 4;

Y 6 LSFLLMGTFLSVQTVLAQLDALLVPPGVAQLSCTLSPQHVTIRDYGV 54
b 8 LTLITQGTG-SWAQSALTQPAVSVSGSPGSIISCTGSSDVGGYNY-VSWVQSPGTAP 65
Y 66 RYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISVPQEDDADYY 116
b 66 KLMTY-----EVSNRPSGVNRFSGSK--SGNTASLTISGLQADDEADYY 110

RESULT 8
US-10-039-785-49
Sequence 49, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 49
LENGTH: 245
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: T1014G04 scFv
US-10-039-785-49

Query Match 28.5%; Score 187; DB 4; Length 245;
Best Local Similarity 37.7%; Pred. No. 2.8e-12;
Matches 46; Conservative 18; Mismatches 34; Indels 24; Gaps 4;

QY 12 GTFLSVS-----QTVLAQLDALLVPPGVAQLSCTLSPQHVTIRDYGV 54
DB 111 GTLVTVSSGGGGGGGGGSAQPVLTQPPGASGSPGSIISCTGSSDVGSVEY-V 169
QY 55 SWYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISVPQEDDADYY 114
DB 170 SWYQHPGKAPRLMI-----SEVNKRPSGVNRFSGSK--SGNTASLTISGLQADDEADYY 223
QY 115 CS 116
DB 224 CS 225

RESULT 9
US-08-793-450-6
Sequence 6, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHABEIH, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-793-450-6

Query Match 28.4%; Score 186.5; DB 4; Length 238;
Best Local Similarity 37.8%; Pred. No. 3.1e-12;
Matches 45; Conservative 21; Mismatches 42; Indels 11; Gaps 4;
Y 1 MACRCUSFILMGTFESV-SQTVLAQDALLVPPGQVAQLSCTISPOHVTIRDYGVSWYQQ 59
b 1 MGWSCILFLVATGTVHSDIELTQDPAVSVALGQTVRIIC---QGDSLRITYASWYQQ 56
Y 60 RAGSAFVLYLXRSSEEDHRRPADIDPESAAKDEAHNACVLTISPVQPEDDADYCVSG 118
b 57 KPGCAPVLYGK---NNRPSGIDRISGS--SSGNTASITITGAQAEADYDFCNSG 109

RESULT 10
US-09-025-769B-34
; Sequence 34, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-34

Query Match 28.3%; Score 186; DB 4; Length 107;
Best Local Similarity 41.2%; Pred. No. 1.3e-12;
Matches 42; Conservative 15; Mismatches 35; Indels 10; Gaps 3;
QY 22 LAQDALLVPPGQVAQLSCTISPOHVTIRDYGVSWYQAGSAPRYLLYYRSEEDHRRPA 81

Db 4 LTQPPSVSVAPGQTARISCSGD-----ALGDKVASWYQKPGCAPVLYI-----DDSDRPS 55
QY 82 DIPDRSAKDEAHNACVLTISPVQPEDDADYCVSGYGFSP 123
Db 56 GIPERFSGS--NSGNTATLTISGTQAEADYCVQQRHYTTPP 95

RESULT 11
US-09-025-769B-55
; Sequence 55, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-55

Query Match 28.3%; Score 186; DB 4; Length 107;
Best Local Similarity 41.2%; Pred. No. 1.3e-12;
Matches 42; Conservative 15; Mismatches 35; Indels 10; Gaps 3;
QY 22 LAQDALLVPPGQVAQLSCTISPOHVTIRDYGVSWYQAGSAPRYLLYYRSEEDHRRPA 81
Db 4 LTQPPSVSVAPGQTARISCSGD-----ALGDKVASWYQKPGCAPVLYI-----DDSDRPS 55
QY 82 DIPDRSAKDEAHNACVLTISPVQPEDDADYCVSGYGFSP 123
Db 56 GIPERFSGS--NSGNTATLTISGTQAEADYCVQQRHYTTPP 95

RESULT 12
US-08-665-202-39
; Sequence 39, Application US/08665202
; Patent No. 597322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 13-JUN-1996
 CLASSIFICATION: 424
 APPLICATION NUMBER: US 08/665,202
 PRIORITY APPLICATION DATA:
 FILING DATE: 14-JUN-1995
 APPLICATION NUMBER: US 60/000,238
 PRIORITY APPLICATION DATA:
 FILING DATE: 15-JUN-1995
 APPLICATION NUMBER: US 60/000,250
 PRIORITY APPLICATION DATA:
 FILING DATE: 13-JUN-1996
 APPLICATION NUMBER: US 08/665,202
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061410
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-09-315-574-39

Query Match 28.3%; Score 186; DB 2; Length 112;
 Best Local Similarity 41.8%; Pred. No. 1.4e-12;
 Matches 41; Conservative 21; Mismatches 28; Indels 8; Gaps 4;
 19 QTVLAQDALLVFPQVQAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 78
 1 QSVLTQPPSVSAAPGQKVTISCSGSSNIG-NNY-VSWYQQLFGTAPKLLIY----SDNQ 54
 79 RPADIPDRFSAKDEAHNACVLITISPVQPEDDADYYCS 116
 55 RPSGVDPDRFSGSK--SGTSASLAISGLRSEDEADYYCA 90

RESULT 13

US-09-315-574-39
 ; Sequence 39, Application US/09315574
 ; Patent No. 6512097
 ; GENERAL INFORMATION:
 ; APPLICANT: Marks, James D.
 ; APPLICANT: Schier, Robert
 ; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
 ; TITLE OF INVENTION: Tumor Antigens
 ; NUMBER OF SEQUENCES: 141
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
 ; STREET: Four Embarcadero Center, Suite 1100
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4106
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

RESULT 14

US-08-305-683A-4
 ; Sequence 4, Application US/08305683A
 ; Patent No. 5646041
 ; GENERAL INFORMATION:
 ; APPLICANT: HARFELDT, Elisabeth
 ; APPLICANT: LAKE, Philip
 ; APPLICANT: NOTTAGE, Barbara
 ; APPLICANT: OSTBERG, Lars G.
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX
 ; TITLE OF INVENTION: VIRUS AND CELL LINE PRODUCING THE SAME
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/305,683A
 ; FILING DATE: 13-SEP-1994
 ; CLASSIFICATION: 424

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 20-MAY-99
 CLASSIFICATION: 530
 APPLICATION NUMBER: US 60/000,238
 PRIORITY APPLICATION DATA:
 FILING DATE: 14-JUN-1995
 APPLICATION NUMBER: US 60/000,250
 PRIORITY APPLICATION DATA:
 FILING DATE: 15-JUN-1995
 APPLICATION NUMBER: US 08/665,202
 FILING DATE: 13-JUN-1996
 APPLICATION NUMBER: US 08/665,202
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061411
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-315-574-39

Query Match 28.3%; Score 186; DB 4; Length 112;
 Best Local Similarity 41.8%; Pred. No. 1.4e-12;
 Matches 41; Conservative 21; Mismatches 28; Indels 8; Gaps 4;
 19 QTVLAQDALLVFPQVQAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 78
 1 QSVLTQPPSVSAAPGQKVTISCSGSSNIG-NNY-VSWYQQLFGTAPKLLIY----SDNQ 54
 79 RPADIPDRFSAKDEAHNACVLITISPVQPEDDADYYCS 116
 55 RPSGVDPDRFSGSK--SGTSASLAISGLRSEDEADYYCA 90

RESULT 14

US-08-305-683A-4
 ; Sequence 4, Application US/08305683A
 ; Patent No. 5646041
 ; GENERAL INFORMATION:
 ; APPLICANT: HARFELDT, Elisabeth
 ; APPLICANT: LAKE, Philip
 ; APPLICANT: NOTTAGE, Barbara
 ; APPLICANT: OSTBERG, Lars G.
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX
 ; TITLE OF INVENTION: VIRUS AND CELL LINE PRODUCING THE SAME
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/305,683A
 ; FILING DATE: 13-SEP-1994
 ; CLASSIFICATION: 424

PRIOR APPLICATION DATA: US 07/759,279
APPLICATION NUMBER: 13-SEP-1991
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
JS-08-0305-683A-4

Query Match	28.1%	Score 184.5;	DB 1;	Length 131;
Best Local Similarity	42.0%;	Pred. NO. 2.4e-12;		
Matches	42;	Conservative 19;	Mismatches 32;	Indels 7; Gaps 3;
2y	16	SVSQVTVAQLDALLVFFGQVAQLSCTLSPOHTIRDYCVSWYQOAGSAPRLLLYRSEE	75	
2b	17	SMAQSVLTQPPSVSGAPGQGYTLCSTGSRNSIG-AGYDVHWYQHLPGTAPKLLY----	71	
2y	76	DHRRPADIPDRFSAKDEAHNACVLTIISVQPEDDADYYC	115	
2b	72	DNNRSGVPDPAFSGSK--SGTSASLAIITGLQAEDEADYYC	109	

RESULT 15
 US-09-025-769B-32
 ; Sequence 32, Application US/09025759B
 ; Patent No. 6300064
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plusekthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-32

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Query March          27.9%; Score 183; DB 4; Length 109;
Best local similarity 40.0%; Pred. No. 2.8e-12;
Matches 42; Conservative 22; Mismatches 33; Indels 8; Gaps 4;

QY      19 QTVLAQLDALLVFGQAQLGSLTSPQHVTIRDYGVSWYQQRAAGAPRYLLYYRSEDDHH 78
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
DB      1   QSVLTQPVSFSGAGPGRVITISCGSSSNG-SNY-VSWYQLPLGPSTAPKLLI---DNNQ 54

QY      79 RPADIPRFSAAGDEAHNAVCVITISVPQEDDADYCVSGVGFSF 123
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
DB      55 RPSGVPRFRGSK--SGTGAALATGCLOSEDRADYVCOOHVTPP 97

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Search completed: February 9, 2004, 12:49:04
Job time : 15.5135 secs


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Query Match      43.4%; Score 233.5; DB 2; Length 142;
Best Local Similarity 54.7%; Pred. NO. 5.8e-17;
Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

Y 9 GOVAQLSCTLSFQVHTIRDTGVSWYQQRAGSAPRYLLYYRSEEDHRRPADIPDRFSAKD 68
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 GATIRLSCTLSNDH-NIGIYSIYVYQQRGHPFRLLRYFSHSDKHQGDIPDRFSGSKD 92
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Y 69 EAHNACVLITSPVQEDDADYCVSG 94
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 TARNLGYLSISELQPEDEAVYCAVG 118
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
A28344
VpreB protein precursor - mouse
;Species: Mus musculus (house mouse)
;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
;Accession: A28344
;X:Kudo, A.; Melchers, F
EMBO J. 6, 2267-2272, 1987
A>Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se
A|Reference number: A91077; MUID:88029315; PMID:3117530
A|Accession: A28344
A|Molecule type: DNA
A|Residues: 1-142 <KUD>
A|Cross-references: GB:X05556; GB:Y00079; NID:G55409; PIDN:CAA29071.1; PID:G55410
A|Note: the authors translated the codon GAG for residue 110 as Gln
A|Superfamily: immunoglobulin V region; immunoglobulin homology
F120-142/Product: VpreB protein #status Predicted <NAI>

Query Match      42.7%; Score 229.5; DB 2; Length 142;
Best Local Similarity 53.5%; Pred. NO. 1.5e-16;
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;

Y 9 GOVAQLSCTLSFQVHTIRDTGVSWYQQRAGSAPRYLLYYRSEEDHRRPADIPDRFSAKD 68
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 GATIRLSCTLSNDH-NIGIYSIYVYQQRGHPFRLLRYFSHSDKHQGDIPDRFSGSKD 92
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Y 69 EAHNACVLITSPVQEDDADYCVSG 94
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 TTRNLGYLSISELQPEDEAVYCAVG 118
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
A28258
VpreB protein - human
;Species: Homo sapiens (man)
;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Nov-1999
;Accession: S00258
;X:Baue, S.R.; Kudo, A.; Melchers, F.
EMBO J. 7, 111-116, 1988
A>Title: Structure and pre-B lymphocyte restricted expression of the VpreB gene in human
A|Reference number: S00258; MUID:88156069; PMID:3258819
A|Accession: S00258
A|Molecule type: DNA
A|Residues: 1-139 <BAU>
A|Cross-references: EMBL:M34927; NID:G340304; PIDN:AAA61292.1; PID:G340305
C|Genetics:
A|Gene: GDB:VPREB1
A|Cross-references: GDB:120493; OMIM:146770
A|Map position: 22q11.2-22q11.2
A|Introns: 16/1
C|Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match      38.6%; Score 207.5; DB 2; Length 139;
Best Local Similarity 48.8%; Pred. NO. 2.7e-14;
Matches 42; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

Y 9 GOVAQLSCTLSFQVHTIRDTGVSWYQQRAGSAPRYLLYYRSEEDHRRPADIPDRFSAKD 68
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 GTTIRLTCLANDH-DIGVYSVVYQQRGHPFRLLRYFSOSDKSGOVPPRPFSGSKD 92
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


A; Introns: 17/1

Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin
1-20/Domain: signal sequence #status predicted <SIG>
21-120/Product: Ig lambda chain V-II region #status predicted <MAT>
Query Match 34.3%; Score 184.5; DB 2; Length 120;
Best Local Similarity 44.7%; Pred. No. 5.4e-12;
Matches 39; Conservative 13; Mismatches 29; Indels 5; Gaps 2;
9 GQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIPDRFSAKD 68
35 GSSAKLTCTLSAHT---YIIWYQQQGEAPRYLMQLKSDGYTKGTGVPDRFSGSS 91
69 EAHNACVLTISPVQPEDDADYCSV 93
92 GADR--YLIISVQADDEADYICGV 114
RESULT 15
16848
3 lambda chain V-II region precursor - human
Species: Homo sapiens (man)
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
Accession: S60297; S16848
Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Muncl. Lett. 34, 57-62, 1992
Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm
Reference number: S60295; MUID:93122853; PMID:1282498
Accession: S60297
Status: preliminary
Molecule type: DNA
Residues: 1-136 <KU2>
Cross-references: EMBL:X62125; NID:g38334; PIDN:CAA44056.1; PID:g38335
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin
34-111/Domain: immunoglobulin homology <IMM>
Query Match 34.3%; Score 184.5; DB 2; Length 136;
Best Local Similarity 45.9%; Pred. No. 6.2e-12;
Matches 39; Conservative 14; Mismatches 25; Indels 7; Gaps 3;
8 PGQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIPDRFSAK 67
33 PGQSVTISCTGTSSDVQAINY-VSWYQHHPGKAPKLMYEVSE----RPSGVDRFRSGSK 87
68 DEAHNACVLTISPVQPEDDADYCS 92
88 --SGNTASLTVSGLOAEADYICT 110
earch completed: February 9, 2004, 12:46:33
ob time : 14.7162 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

un on: February 9, 2004, 12:31:07, Search time 9.36487 Seconds
(without alignments)
497.139 Million cell updates/sec

itle: US-09-981-876-200_copy_25_123

effect score: 538
sequence: 1 LDALLVFGQVQLSCTLSP.....PVQPEDDADYCVGVGFSP 99

coring table: BLOSUM62

Gapop 10.0, Gapext 0.5

earched: 127863 seqs, 47026705 residues

otal number of hits satisfying chosen parameters: 127863

inimum DB seq length: 0

aximum DB seq length: 200000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query Match	Length	DB ID	Description
1	538	100.0	123	1	VPR3 HUMAN	Q9UK13 homo sapien
2	233.5	43.4	142	1	VPR2 MOUSE	P13373 mus musculus
3	229.5	42.7	142	1	VPR1 MOUSE	P13372 mus musculus
4	207.5	38.6	145	1	VPRE HUMAN	P12018 homo sapien
5	200	37.2	111	1	LV6C HUMAN	P06317 homo sapien
6	197	36.6	112	1	LV6A HUMAN	P01721 homo sapien
7	185.5	34.5	111	1	LV2F HUMAN	P01709 homo sapien
8	185	34.4	111	1	LV6E HUMAN	P06318 homo sapien
9	183	34.0	131	1	LV6B HUMAN	P06319 homo sapien
10	182.5	33.9	111	1	LV2L HUMAN	P80422 homo sapien
11	180.5	33.6	111	1	LV2K HUMAN	P04209 homo sapien
12	175.5	32.6	112	1	LV2I HUMAN	P01712 homo sapien
13	175	32.5	111	1	LV2E HUMAN	P01708 homo sapien
14	172.5	32.1	109	1	LV3A HUMAN	P01714 homo sapien
15	171	31.8	108	1	LV3B HUMAN	P01713 homo sapien
16	167.5	31.1	110	1	LV2J HUMAN	P01702 homo sapien
17	167.5	31.1	111	1	LV1D HUMAN	P06316 homo sapien
18	167	31.0	130	1	LV1G HUMAN	P01719 homo sapien
19	165	30.7	108	1	LV5A HUMAN	P04208 homo sapien
20	165	30.7	109	1	LV1F HUMAN	P80748 homo sapien
21	164	30.5	111	1	LV3B HUMAN	P01705 homo sapien
22	163.5	30.4	111	1	LV2H HUMAN	P01711 homo sapien
23	163.5	30.4	111	1	LV2B HUMAN	P01718 homo sapien
24	162	29.9	106	1	LV4D HUMAN	P01716 homo sapien
25	161	29.9	109	1	LV4B HUMAN	P01622 homo sapien
26	161	29.9	109	1	KV3D HUMAN	P01717 homo sapien
27	160	29.7	107	1	KV3A HUMAN	P01619 homo sapien
28	160	29.7	108	1	LV3A HUMAN	P04211 homo sapien
29	159.5	29.6	117	1	LV0A HUMAN	P01715 homo sapien
30	158	29.4	106	1	LV4A HUMAN	P18135 homo sapien
31	158	29.4	129	1	KV3L HUMAN	P01620 homo sapien
32	156	29.0	109	1	KV3B HUMAN	P04206 homo sapien
33	156	29.0	109	1	KV3G HUMAN	

34	155.5	28.9	112	1	LV1H HUMAN	P06887 homo sapien
35	154.5	28.7	111	1	LV2A HUMAN	P01704 homo sapien
36	154.5	28.7	111	1	LV2C HUMAN	P01706 homo sapien
37	154.5	28.7	112	1	LV1B HUMAN	P01700 homo sapien
38	153.5	28.5	111	1	LV2D HUMAN	P01707 homo sapien
39	153	28.4	111	1	LV1C HUMAN	P01701 homo sapien
40	152	28.3	112	1	LV6B HUMAN	P01722 homo sapien
41	152	28.3	129	1	KV3M HUMAN	P18136 homo sapien
42	148	27.5	100	1	KV3C HUMAN	P01621 homo sapien
43	147.5	27.4	109	1	KV3E HUMAN	P01623 homo sapien
44	147	27.3	109	1	LV1E HUMAN	P06888 homo sapien
45	146	27.1	106	1	LV4E HUMAN	P06889 homo sapien

ALIGNMENTS

RESULT 1
VPR3_HUMAN
ID VPR3_HUMAN STANDARD; PRT; 123 AA.
AC Q9UK13;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pre-B lymphocyte protein 3 precursor (VpreB3 protein) (NZ7C7-2).
GN VPREB3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20169186; PubMed=10702669;
RX Rosnet O., Mattei M.-G., Delattre O., Schiff C.;
RA "VPREB3: cDNA characterization and expression in human and chromosome
RT mapping in human and mouse."
RL Cytogenet. Cell Genet. 87:205-208(1999).
[2]
RN SEQUENCE FROM N.A.
RP Shimizu N., Minosima S., Kawasaki K., Sasaki T., Hosono K.;
RA "Molecular cloning of NZ7C7-2 gene."
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
TX TISSUE=Testis;
MD MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN B CELL PRECURSORS. EXPRESSED IN
FETAL LIVER, BONE MARROW, SPLEEN, AND LYMPH NODE.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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C or send an email to license@isb-sib.ch).

C -----
R EMBL; AF163825; AAF09451.1; -
R EMBL; AB050772; BAB83034.1; -
R EMBL; BC020666; BAH20666.1; -
R HSSP; P01709; 2MCG; VPREB3.
R Genew; HGNC:12710; VPREB3.
R MIM; 605017; -
R InterPro; IPR007110; IG-like.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; IG_1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS0835; IG_LIKE; 1.
R Immunoglobulin domain; B-cell; Signal.
R SIGNAL 1 20 POTENTIAL.
R CHAIN 21 123 PRE-B LYMPHOCYTE PROTEIN 3.
R DOMAIN 21 123 IG-LIKE.
R DISULFID 40 115 BY SIMILARITY.
R SEQUENCE 123 AA; 13710 MW; BF09AC5196059E85 CRC64;

Query Match 100.0%; Score 538; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 LDALLVFPQVQAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYRSEEDHHRPADIP 60

2b 25 LDALLVFPQVQAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYRSEEDHHRPADIP 84

2y 61 DRFSAKDEAHNACVLTISPQPEDDADYCSVGSP 99

2b 85 DRFSAKDEAHNACVLTISPQPEDDADYCSVGSP 123

RESULT 2

ID_VPR1_MOUSE STANDARD; PRT; 142 AA.
AC P13372;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Immunoglobulin omega chain precursor (VpreB1 protein).
GN VPREB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2J;
RX MEDLINE=88029315; PubMed=3117530;
RA Kudo A., Melchers F.;
RT "A second gene, VpreB in the lambda 5 locus of the mouse, which
RT appears to be selectively expressed in pre-B lymphocytes.";
RL EMBO J. 6:2267-2272(1987).
CC -1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC STEPS OF B-CELL DIFFERENTIATION.
CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; X05563; CAA29077.1; -
DR PIR; B28344; B28344.
DR HSSP; P01607; IREI.
DR MGD; MGI:98937; VpreB2.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR Immunoglobulin domain; B-cell; Signal.
DR SIGNAL 1 19 POTENTIAL.
DR CHAIN 20 142 IMMUNOGLOBULIN OMEGA CHAIN.
DR DOMAIN 20 41 FRAMEWORK-1.
DR DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.
DR DOMAIN 57 70 FRAMEWORK-2.
DR DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.
DR DOMAIN 82 115 FRAMEWORK-3.
DR DISULFID 41 115 BY SIMILARITY.
R SEQUENCE 142 AA; 16052 MW; 7EA7128A4E63D920 CRC64;

Query Match 43.4%; Score 233.5; DB 1; Length 142;
Best Local Similarity 54.7%; Pred. No. 2.4e-18;
Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

Qy 9 GQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYRSEEDHHRPADIPDRFSAKD 68

Db 34 GATIRLSCTLSNDH-NIGIYIYVQORPGHPFRLRYFSHSDKHGQDIPPRFSGSKD 92

Qy 69 EAHNACVLTISPQPEDDADYCSVG 94

Db 93 TARNLYLSISELQFEDAVYCAVG 118

RESULT 3

ID_VPR1_MOUSE STANDARD; PRT; 142 AA.
AC P13372;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Immunoglobulin iota chain precursor (VpreB1 protein).
GN VPREB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2J;
RX MEDLINE=88029315; PubMed=3117530;
RA Kudo A., Melchers F.;
RT "A second gene, VpreB in the lambda 5 locus of the mouse, which
RT appears to be selectively expressed in pre-B lymphocytes.";
RL EMBO J. 6:2267-2272(1987).
CC -1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC STEPS OF B-CELL DIFFERENTIATION.
CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

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C or send an email to license@isb-sib.ch).

EMBL; X05556; CAA29071.1; -.
EMBL; X05557; CAA29072.1; -.
PIR; A28344; A28344.
HSP; P01607; IRE1.
MGD; MGI:98936; Vpreb1.
GO; GO:0005886; C:plasma membrane; IPI.
GO; GO:0004872; P:receptor activity; IPI.
GO; GO:0030097; P:hemoipoiesis; IPI.
GO; GO:0006955; P:immune response; IPI.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin domain; B-cell; Signal.
SIGNAL 1 19 POTENTIAL.
CHAIN 20 142 IMMUNOGLOBULIN IOTA CHAIN.
DOMAIN 20 41 FRAMEWORK-1.
DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.
DOMAIN 57 70 FRAMEWORK-2.
DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.
DOMAIN 82 115 FRAMEWORK-3.
DISULFID 41 115 BY SIMILARITY.
SEQUENCE 142 AA; 16125 MW; 2E18BF963A0F448C CRC64;
Query Match 42.7%; Score 229.5; DB 1; Length 142;
Best Local Similarity 53.5%; Pred. No. 6.4e-18;
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;
Y 9 GQVQLSTLSQPHVTIRDYGVSVYQORAGSAPRYLLYRSSEDRHRPADIPDRSAKD 68
b 34 GATIRLSTLNDH-NIGTIVSYWYQORPGHPFRFLRYFSHDKHGDPDIPRFGSKD 92
Y 69 EAHNACVLITSPQVEDDADYCSVG 94
b 93 TTRNLGYLSISELOPEADYVYCAVG 118
RESULT 4
PRE HUMAN STANDARD; PRT; 145 AA.
D VPRE_HUMAN
C P12018;
T 01-OCT-1999 (Rel. 12, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
E Immunoglobulin Iota chain precursor (V(pre)B protein) (VpreB protein)
E (CD179a antigen).
N VPREB1 OR VPRESB.
X Homo sapiens (Human).
X Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
UN [1]
UN SEQUENCE FROM N.A.
X MEDLINE=95021318; PubMed=7935499;
X Quelipa-Fonlupt V., Bossy D., Alkari P., Fumoux F., Fougereau M.,
X Schaff C.;
X "The human pre-B cell receptor: structural constraints for a tentative
X model of the pseudo-light (psi L) chain.";
X Mol. Immunol. 31:1099-1108(1994).
X [2]
X [3]
X MEDLINE=97228902; PubMed=9074928;
X Kawasaki K., Minoshima S., Mine E., Shibuya K., Shintani A.,
X Schmeits J.L., Wang J., Shimizu N.;
X "One-megabase sequence analysis of the human immunoglobulin lambda
X gene locus.";
X Genome Res. 7:250-261(1997).
X [3]
X MEDLINE=88196069; PubMed=3258819;
X Bauer S.R., Kudo A., Melchers F.;
X 19 lambda chain V-VI region SUT.

RT X05556; CAA29071.1; -.
RT X05557; CAA29072.1; -.
RT A28344; A28344.
RL HSP; P01607; IRE1.
RL MGD; MGI:98936; Vpreb1.
CC GO; GO:0005886; C:plasma membrane; IPI.
CC GO; GO:0004872; P:receptor activity; IPI.
CC GO; GO:0030097; P:hemoipoiesis; IPI.
CC GO; GO:0006955; P:immune response; IPI.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003596; IG_V.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC Immunoglobulin domain; B-cell; Signal.
CC SIGNAL 1 19 POTENTIAL.
CC CHAIN 20 142 IMMUNOGLOBULIN IOTA CHAIN.
CC DOMAIN 20 41 FRAMEWORK-1.
CC DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 57 70 FRAMEWORK-2.
CC DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 82 115 FRAMEWORK-3.
CC DISULFID 41 115 BY SIMILARITY.
CC SEQUENCE 142 AA; 16125 MW; 2E18BF963A0F448C CRC64;
Query Match 42.7%; Score 229.5; DB 1; Length 142;
Best Local Similarity 53.5%; Pred. No. 6.4e-18;
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;
Y 9 GQVQLSTLSQPHVTIRDYGVSVYQORAGSAPRYLLYRSSEDRHRPADIPDRSAKD 68
b 34 GATIRLSTLNDH-NIGTIVSYWYQORPGHPFRFLRYFSHDKHGDPDIPRFGSKD 92
Y 69 EAHNACVLITSPQVEDDADYCSVG 94
b 93 TTRNLGYLSISELOPEADYVYCAVG 118
RESULT 4
PRE HUMAN STANDARD; PRT; 145 AA.
D VPRE_HUMAN
C P12018;
T 01-OCT-1999 (Rel. 12, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
E Immunoglobulin Iota chain precursor (V(pre)B protein) (VpreB protein)
E (CD179a antigen).
N VPREB1 OR VPRESB.
X Homo sapiens (Human).
X Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
UN [1]
UN SEQUENCE FROM N.A.
X MEDLINE=95021318; PubMed=7935499;
X Quelipa-Fonlupt V., Bossy D., Alkari P., Fumoux F., Fougereau M.,
X Schaff C.;
X "The human pre-B cell receptor: structural constraints for a tentative
X model of the pseudo-light (psi L) chain.";
X Mol. Immunol. 31:1099-1108(1994).
X [2]
X [3]
X MEDLINE=97228902; PubMed=9074928;
X Kawasaki K., Minoshima S., Mine E., Shibuya K., Shintani A.,
X Schmeits J.L., Wang J., Shimizu N.;
X "One-megabase sequence analysis of the human immunoglobulin lambda
X gene locus.";
X Genome Res. 7:250-261(1997).
X [3]
X MEDLINE=88196069; PubMed=3258819;
X Bauer S.R., Kudo A., Melchers F.;
X 19 lambda chain V-VI region SUT.

"Structure and pre-B lymphocyte restricted expression of the VpreB in humans and conservation of its structure in other mammalian species.";
EMBO J. 7;111-116(1988).
-!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY STEPS OF B-CELL DIFFERENTIATION.
-!- SUBUNIT: Associates non-covalently with IGLL1.
-!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- DATABASE: NAME=PROV; NOTE=PROV 1:59-63(2000).
WWW="http://www.ncbi.nlm.nih.gov/prov/guide/574153212.g.htm".
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EMBL; D86992; BAA19887.1; -.
EMBL; D88270; BAA20030.1; -.
EMBL; S74019; AAB32118.1; -.
EMBL; M34927; AAB61292.1; -.
PIR; I57832; I57832.
PIR; S00258; S00258.
HSP; P80748; 2LOI.
GeneW; HGNC:12709; VPREB1.
MIM; 605141.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
PIfam; PF00047; IG; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin domain; B-cell; Signal; Antigen.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 145 IMMUNOGLOBULIN IOTA CHAIN.
FT DOMAIN 20 41 FRAMEWORK-1.
FT DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 70 FRAMEWORK-2.
FT DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 115 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT CONFLICT 10 10 L -> H (IN REF. 3).
SQ SEQUENCE 145 AA; 16605 MW; 197665B13AF6D46 CRC64;
Query Match 38.6%; Score 207.5; DB 1; Length 145;
Best Local Similarity 48.8%; Pred. No. 1.6e-15;
Matches 42; Conservative 12; Mismatches 31; Indels 1; Gaps 1;
QY 9 GQVQLSTLSQPHVTIRDYGVSVYQORAGSAPRYLLYRSSEDRHRPADIPDRSAKD 68
Db 34 GATIRLSTLNDH-NIGTIVSYWYQORPGHPFRFLRYFSHDKHGDPDIPRFGSKD 92
QY 69 EAHNACVLITSPQVEDDADYCSVG 94
Db 93 VARNEGYSLSISELOPEADYVYCAVG 118
RESULT 5
LV6C_HUMAN
ID LV6C_HUMAN STANDARD; PRT; 111 AA.
AC P06317;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 19 lambda chain V-VI region SUT.

```

DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPRO07110; Ig-like.
DR InterPro; IPRO03006; Ig_MHC.
DR InterPro; IPRO03596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Amyloid.
DR DOMAIN 1 107 IG-LIKE.
DR NON_TER 112 112
DR SEQUENCE 112 AA; 11918 MW; 570BCD9A368BF1FE CRC64;

Query Match 36.6%; Score 197; DB 1; Length 112;
Best Local Similarity 47.6%; Pred. No. 1.6e-14;
Matches 40; Conservative 15; Mismatches 23; Indels 6; Gaps 2;

QY 8 PGQVAQLSCTLSFGHVTIRDYGVSMTQQAGAPRYLLYRSEDDHRRPADIPDRFSAAK 67
14 PKVTVTSCGSGG--SIADSFQWYQKQPGSAPTIVY----DDNQKPSGVDRFSGSI 67

Db 68 DEAHNACVLITSPVQPEDDADYYC 91
68 DDSANSASLATISGLKTEDEADYYC 91

```

DI	15 lambda chain V-12, basic annotation update,
DE	19 lambda chain V-II region MGC.
OS	Os Homo sapiens (Human).
OS	Os Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
[1]_RN	
RN	SEQUENCE.
RP	MEDLINE=75013804; PubMed=4415202;
RX	Fett J.W., Deutsch H.F.;
RA	"Primary structure of the Mcg lambda chain."
RL	Biochemistry 13:4102-4114 (1974).
RL	121

LAMBDA CHAIN GENES.
 MEDLINE:76093781; PubMed=912801;
 RA Felt J.W., Deutsch H.F.;
 RA "A new lambda-chain gene.";
 RN Immunochimistry 12:643-652(1975).
 RL [3]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
 RA Fandgiotopoulos N.;
 RA "Rotational allomerism and divergent evolution of domains in
 RT immunoglobulin light chains.";
 RL Biochemistry 14:3953-3961(1975).
 RL [4]
 RP X-RAY CRYSTALLOGRAPHY.
 RA MEDLINE:90133913; PubMed=2515285;
 RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
 RA "Three-dimensional structure of a light chain dimer crystallized in
 RT water. Conformational flexibility of a molecule in two crystal
 RT forms.";
 RL J. Mol. Biol. 210:601-615(1989).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC -1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
 CC A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
 CC SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
 CC MARKERS.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR FIR; A90381; L2HUMC.
 DR PDB; 2MCG; 15-JUL-92.

```

PDB: 1A8J; 17-JUN-98.
PDB: 1DCL; 15-MAY-97.
GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; F:antigen binding activity; NAS.
GO: GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin V region;
PFam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin V region; Hence-Jones protein; 3D-structure;
Pyroglutamate carboxylic acid.
IG-LIKE.
PYROGLUTAMATE CARBOXYLIC ACID.
BY SIMILARITY.
MOD RES 1 1
DISULFID 22 90
STRAND 5 5
STRAND 10 12
STRAND 18 23
TURN 26 32
TURN 36 40
TURN 42 43
TURN 50 51
TURN 52 54
TURN 55 55
TURN 62 63
TURN 66 68
TURN 72 77
TURN 82 84
STRAND 86 93
STRAND 99 101
STRAND 105 109
STRAND 111 111
NON TER 111 111
SEQUENCE 111 AA; 11558 MW; 7CCID6E2FA3377BA CRC64;

Query Match 34.5%; Score 185.5; DB 1; Length 111;
Best Local Similarity 47.6%; Pred. No. 2.8e-13;
Matches 40; Conservative 14; Mismatches 23; Indels 7; Gaps 3;

Y 9 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAKD 68
b 15 GQSVTISCTGSSG--SIGSNYVQVYQQRPGSAPTNIY---ENNRQPSVEVDRFSGSI 67
Y 69 EAHNACVLTISPQPEDDADYCS 92
b 69 -SGNTASLTISGLQAEDEADYCS 91

RESULT 8
LV6E HUMAN STANDARD; PRT; 111 AA.
AC P06318;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region WLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86122667; PubMed=4089539;
RA Dulet F.E., Strako K., Benson M.D.;
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein
RL (WLT).";
RL Scand. J. Immunol. 22:653-660 (1985).
DR PIR; A01989; L6HULT.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
PFam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 41
FT DOMAIN 20 41
FT DOMAIN 42 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 110
FT DOMAIN 111 118
FT DOMAIN 119 131
FT DISULFID 41 110
FT NON TER 131 131
SEQUENCE 131 AA; 14147 MW; 92A9179C8C05C2CD CRC64;

DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR PFam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 22
FT DOMAIN 23 35
FT DOMAIN 36 50
FT DOMAIN 51 57
FT DOMAIN 58 91
FT DOMAIN 92 101
FT DOMAIN 102 111
FT DISULFID 22 91
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE37BCE24F CRC64;

Query Match 34.4%; Score 185; DB 1; Length 111;
Best Local Similarity 45.2%; Pred. No. 3.1e-13;
Matches 38; Conservative 16; Mismatches 24; Indels 6; Gaps 2;

QY 8 PQVQAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAK 67
DB 14 PEKVTITISCTGSSG--SIGSNYVQVYQQRPGSAPTNIY---ENNRQPSVEVDRFSGSI 67
QY 68 DEAHNACVLTISPQPEDDADYCS 91
DB 68 DSSNSASLTISGLQAEDEADYCS 91

RESULT 9
LV6E HUMAN STANDARD; PRT; 131 AA.
AC P06319;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region EB4 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85215660; PubMed=3923440;
RA Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT "Cloning and sequence analysis of an Ig lambda light chain mRNA
RL expressed in the Burkitt's lymphoma cell line EB4.";
RL Nucleic Acids Res. 13:2931-2941 (1985).
DR PIR; A01990; L6HUEB.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
PFam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 41
FT DOMAIN 20 41
FT DOMAIN 42 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 110
FT DOMAIN 111 118
FT DOMAIN 119 131
FT DISULFID 41 110
FT NON TER 131 131
SEQUENCE 131 AA; 14147 MW; 92A9179C8C05C2CD CRC64;

```

Query Match 34.0%; Score 183; DB 1; Length 131;
Best Local Similarity 45.2%; Pred. No. 6.2e-13;
Matches 38; Conservative 13; Mismatches 27; Indels 6; Gaps 2;

Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIDPRFSAK 67
b 33 PGKVTITSTCT--GNGSITASNTVQYQRRVSAPTIVY----EDNQRLGVDPDFSGSI 86
Y 69 DEAHNAVLITISVPQEDDADYYC 91
b 87 DSSNSGASLTISGLKTEADYYC 110

RESULT 10
LV2L HUMAN
ID LV2L HUMAN STANDARD; PRT; 111 AA.
AC P0422;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG gamma lambda chain V-II region DOT.
DS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 33.9%; Score 182.5; DB 1; Length 111;
Best Local Similarity 47.6%; Pred. No. 5.9e-13;
Matches 40; Conservative 12; Mismatches 25; Indels 7; Gaps 3;

Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIDPRFSAK 67
b 14 PGQAVITSTGLPS-VYDDNFVSWYQTPGAPRLIY----DSDLRPGVDFRFSGSK 68
Y 68 DEAHNAVLITISVPQEDDADYYC 91
b 69 SDTKAA--LTISGLQPDDEATYFC 90

RESULT 11
LV2G HUMAN
ID LV2G HUMAN STANDARD; PRT; 111 AA.
AC P0170;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region BO.
DS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 33.6%; Score 180.5; DB 1; Length 111;
Best Local Similarity 44.7%; Pred. No. 9.6e-13;
Matches 39; Conservative 14; Mismatches 26; Indels 7; Gaps 3;

Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIDPRFSAK 67
b 14 PGQSVTISCTGTSSDVGDKY-VSWYQHPGAPKLIVF---EVSQRPVGVDFRFSGSK 68
Y 68 DEAHNAVLITISVPQEDDADYYCS 92
b 69 SD--NTASITVSGLRADADYYCS 91

RESULT 12
LV2K HUMAN
ID LV2K HUMAN STANDARD; PRT; 112 AA.
AC P04209;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region NIG-84.
DS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 33.6%; Score 180.5; DB 1; Length 111;
Best Local Similarity 44.7%; Pred. No. 9.6e-13;
Matches 39; Conservative 14; Mismatches 26; Indels 7; Gaps 3;

Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIDPRFSAK 67
b 14 PGQSVTISCTGTSSDVGDKY-VSWYQHPGAPKLIVF---EVSQRPVGVDFRFSGSK 68
Y 68 DEAHNAVLITISVPQEDDADYYCS 92
b 69 SD--NTASITVSGLRADADYYCS 91

R Pfam: PF00047; IG: 1.
R SMART: SM00406; IGV: 1.
R PROSITE: PS50835; IG LIKE: 1.
W Immunoglobulin V region; Antyloid; Bence-Jones protein.
I DOMAIN 1 102 IG-LIKE.
I DISULFID 22 90 BY SIMILARITY.
I NON TER 112 112
Q SEQUENCE 112 AA; 11581 MW; 989FEF363AE1E4F3 CRC64;

Query Match 32.6%; Score 175.5; DB 1; Length 112;
Best Local Similarity 47.1%; Pred. No. 3.4e-12;
Matches 40; Conservative 13; Mismatches 25; Indels 7; Gaps 3;

Y 8 PQGVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAK 67
b 14 PQGSITISCTGTSYGVYDF-VSWYQHPGKAPKLIY----DVNGRPSGINSRFGSK 68

Y 68 DEAHNACVLITSPVQPEDDADYCS 92
b 69 --SGNTASLTISGLQAEDEADYCS 91

RESULT 13
V21 HUMAN
D_LV21 HUMAN STANDARD; PRT; 111 AA.
C P01712; 1986 (Rel. 01, Created)
T 21-JUL-1986 (Rel. 01, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
E Ig lambda chain V-II region WIN.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
X NCBI_TaxID=9606;
N SEQUENCE.
P MEDLINE=79062503; PubMed=102365;
X Chen B.L., Chiu Y.-H., Humphrey R.L., Poljak R.J.;
T "Amino acid sequence of the human myeloma lambda chain Win.";
L Biochim. Biophys. Acta 537:9-21(1978).
C -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
R HSP; P01709; 2MCG.
R GO: GO:0005576; C:extracellular; NAS.
R GO: GO:0003823; F:antigen binding activity; NAS.
R GO: GO:0006955; P:immune response; NAS.
R InterPro: IPR007110; IG-like.
R InterPro: IPR003006; IG_MHC.
R Pfam: PF00047; IG_V.
R SMART: SM00406; IGV: 1.
R PROSITE: PS50835; IG LIKE: 1.
W Immunoglobulin V region; Bence-Jones protein;
FT DOMAIN 1 106 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT SITE 91 91
FT NON TER 111 111
FT SEQUENCE 111 AA; 11694 MW; 8C3CE95FE721B87C CRC64;

Query Match 32.5%; Score 175; DB 1; Length 111;
Best Local Similarity 44.9%; Pred. No. 3.8e-12;
Matches 40; Conservative 15; Mismatches 26; Indels 8; Gaps 4;

Y 8 PQGVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAK 67
b 14 PQGSITISCTGTSYGVYDF-VSWYQHPGKAPKLIY----DVNGRPSGINSRFGSK 68

Y 68 DEAHNACVLITSPVQPEDDADYCSVGYG 96
b 69 --SANTASLTISGLQANNEADYCS-SYG 94

RESULT 14
LV2E HUMAN
ID LV2E HUMAN STANDARD; PRT; 109 AA.
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80008606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human IGA1 immunoglobulin. V. Amino acid
sequence of a human IGA lambda light chain (Bur).";
RL J. Biol. Chem. 254:9006-9016(1979).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
MARKERS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01974; L2HUBR.
DR HSP; P01709; 2MCG.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG: 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; IG LIKE: 1.
W Immunoglobulin V region; Pyrrrolidone carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT SITE 91 91
FT NON TER 109 109
FT SEQUENCE 109 AA; 11506 MW; BFD8AE1C5D267FAB CRC64;

Query Match 32.1%; Score 172.5; DB 1; Length 109;
Best Local Similarity 45.2%; Pred. No. 6.9e-12;
Matches 38; Conservative 12; Mismatches 27; Indels 7; Gaps 3;

QY 8 PQGVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAK 67
Db 14 PGHSVTISCTGTSYGVYDF-VSWYQHPGKAPKLIY----EVSRRPSGVDPDRFGSK 68

QY 68 DEAHNACVLITSPVQPEDDADYCYC 91
Db 69 --SGNTASLTISGLQAEDEADYCYC 90

RESULT 15
LV3A HUMAN
ID LV3A HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikier M., Shinoda T., Putnam F.W.;

"The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide bridges."

J. Biol. Chem. 245:2171-2176(1970).
-1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A01980; LSHUSH.

RR HSP; P80748; ZLOI.
RR GO; GO:0005576; C:extracellular; NAS.
RR GO; GO:0003823; F:antigen binding activity; NAS.
RR GO; GO:0006955; P:immune response; NAS.
RR InterPro; IPR007110; Ig-like.
RR InterPro; IPR003006; Ig_MHC.
RR InterPro; IPR003596; Ig_v.
RR Pfam; PF00047; Ig; 1.
RR SMART; SM00406; IGV; 1.
RR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 97 IG-LIKE.

FT DISULFID 21 86
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match 31.8%; Score 171; DB 1; Length 108;
Best Local Similarity 42.2%; Pred. No. 9.9e-12;
Matches 38; Conservative 17; Mismatches 25; Indels 10; Gaps 4;
CY 3 ALLVPPGVQVQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDR 62
DB 8 AVSVLGGTVRITC-----QGDSLEGYDAWYQKPGQAPLLVIYGR----NNRPSGIPDR 59
CY 63 FSAAKDEAHNACVLTISVPQEDDADYICS 92
DB 60 FSGS--SSGHTAS-LTITGAQAEADYICN 87

Search completed: February 9, 2004, 12:47:05
Job time : 10.3649 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: February 9, 2004, 12:38:06 / Search time 31.2162 Seconds
(without alignments)
818.395 Million cell updates/sec

file: us-09-981-876-200_copy_25_123

effect score: 538
sequence: 1 LDALLVFEQVAQLSCTLSP.....PVQPEDDADYCVGVGFSP 99

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 830525 seqs, 258052604 residues

total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_prodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	372.5	69.2	123	11 Q61243	Q61243 mus musculus
2	199	37.0	135	4 Q9H524	Q9H524 homo sapien
3	197	36.6	112	4 Q96JD1	Q96JD1 homo sapien
4	193	35.9	112	4 Q96JD2	Q96JD2 homo sapien
5	189.5	35.2	116	4 Q96JD0	Q96JD0 homo sapien
6	175	32.5	237	4 Q8WTU6	Q8WTU6 homo sapien
7	174.5	32.4	236	4 Q96E61	Q96E61 homo sapien
8	172.5	32.1	237	4 Q8WUK4	Q8WUK4 homo sapien
9	172.5	32.1	240	4 Q9NSD6	Q9NSD6 homo sapien
10	169	31.4	107	4 Q9UL86	Q9UL86 homo sapien
11	166	30.9	109	4 Q8TBC9	Q8TBC9 homo sapien
12	165	30.7	233	4 Q8N355	Q8N355 homo sapien
13	161	29.9	234	4 Q8N355	Q8N355 homo sapien
14	161	29.9	235	11 Q99M11	Q99M11 mus musculus
15	160	29.7	108	4 Q96S80	Q96S80 homo sapien
16	158	29.4	109	4 Q9UL78	Q9UL78 homo sapien

17	158	29.4	236	4 Q8NEJ1	Q8NEJ1 homo sapien
18	157	29.2	110	4 Q8TB63	Q8TB63 homo sapien
19	155	28.8	233	4 Q96169	Q96169 homo sapien
20	151.5	28.2	100	6 O77624	O77624 bos taurus
21	151	28.1	101	4 Q81ZD8	Q81ZD8 homo sapien
22	151	28.1	233	4 Q8NSF4	Q8NSF4 homo sapien
23	150.5	28.0	105	4 Q8WVJ6	Q8WVJ6 homo sapien
24	148	27.5	107	4 Q9UL82	Q9UL82 homo sapien
25	138	25.7	132	4 Q8TSD0	Q8TSD0 homo sapien
26	137	25.5	108	4 Q9UL83	Q9UL83 homo sapien
27	135	25.1	234	4 Q8NEK1	Q8NEK1 homo sapien
28	134	24.9	97	4 Q43234	Q43234 homo sapien
29	134	24.9	107	11 Q9ERZ9	Q9ERZ9 mus musculus
30	133.5	24.8	484	11 Q8VEA0	Q8VEA0 mus musculus
31	132	24.5	109	4 Q9UL85	Q9UL85 homo sapien
32	130.5	24.3	99	11 Q9UL74	Q9UL74 mus musculus
33	128	23.8	107	4 Q96SA9	Q96SA9 homo sapien
34	128	23.8	108	4 Q9UL77	Q9UL77 homo sapien
35	127.5	23.7	239	4 Q8NEK0	Q8NEK0 homo sapien
36	127	23.6	108	4 Q9UL79	Q9UL79 homo sapien
37	124.5	23.1	114	4 Q9UL80	Q9UL80 homo sapien
38	124	23.0	494	4 Q96K68	Q96K68 homo sapien
39	123.5	23.0	113	11 Q8CGS1	Q8CGS1 mus musculus
40	123.5	23.0	234	11 Q8R062	Q8R062 mus musculus
41	123.5	23.0	469	11 Q8R3V9	Q8R3V9 mus musculus
42	123	22.9	111	11 Q920E9	Q920E9 mus musculus
43	120.5	22.4	93	4 Q9UL76	Q9UL76 homo sapien
44	120.5	22.4	121	4 Q9UL96	Q9UL96 homo sapien
45	120.5	22.4	239	4 Q8TCD0	Q8TCD0 homo sapien

ALIGNMENTS

RESULT 1

Q61243 ID Q61243 PRELIMINARY; PRT; 123 AA.
AC Q61243; STRAIN=C57BL/6J; TISSUE=Stomach;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE SRS20 protein precursor (Pre-B lymphocyte gene 3).
GN VPRES3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=93259124; PubMed=8491176;
RA Shirasawa T., Ohnishi K., Hagiwara S., Shigemoto K., Takebe Y.,
RA Rajewsky K., Takemori T.,
RT "A novel gene product associated with mu chains in immature B cells.";
RL EMBO J. 12:1827-1834(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Db 67 EDEADYVCGTWHSNS 81

RESULT 3

Q96JD1 PRELIMINARY; PRT; 112 AA.

ID Q96JD1

AC Q96JD1

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-VAR-2003 (TRENBLrel. 23, Last annotation update)

DE Amyloid lambda 6 light chain variable region PIP (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]_SEQUENCE FROM N.A.

RP TISSUE=Bone marrow;

RC Ferrétti V., Casarini S., Colli Vignarelli M., Merlini G.;

RT "Amyloid lambda 6 light chain variable region PIP.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

EMBL; AF267874; AAK58585.1; "

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV_1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 112

FT NON_TER 112

SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match 36.6%; Score 197; DB 4; Length 112;

Best Local Similarity 47.6%; Pred.No 7e-15;

Matches 40; Conservative 14; Mismatches 24; Indels 6;

G

QY 8 PQGVAQLSCTLSPOHVIIRYGVSWTQQRAGSAPVLLYRSEEDHHPAIDPFRF

Db 14 PKGTTTSCRESSG--SIASNYQVYQRRPGSAPTIVY---EDNQRPSPGVDFR

QY 68 DEAHNACVLITSPQVEDDADYIC 91

Db 68 DSSNSASLTISGLKTEDEADYIC 91

RESULT 4

Q96JD2 PRELIMINARY; PRT; 112 AA.

ID Q96JD2

AC Q96JD2

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-VAR-2003 (TRENBLrel. 23, Last annotation update)

DE Amyloid lambda 6 light chain variable region NEG (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]_SEQUENCE FROM N.A.

RP TISSUE=Bone marrow;

RC Ferrétti V., Casarini S., Colli Vignarelli M., Merlini G.;

RT "Amyloid lambda 6 light chain variable region NEG.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

EMBL; AF267873; AAK58585.1; "

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV_1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 112

FT NON_TER 112

SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;


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S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
M Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
N NCBI_TaxID=9606;
P SEQUENCE FROM N.A.
C TISSUE=Tonsil;
A Strausberg R.;
L Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
R EMBL; BC020233; AAH20233.1; -.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; IG; 2.
R SMART; SM00406; IGV; 1.
R PROSITE; PS00290; IG_MHC; 1.
K Hypothetical protein.
W SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;
X SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 32.1%; Score 172.5; DB 4; Length 237;
Best Local Similarity 44.0%; Pred. No. 1.1e-11;
Matches 37; Conservative 15; Mismatches 25; Indels 7; Gaps 3;

2y . 8 PQGVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAK 67
2b 33 PQGRTVISTGSSNIG-AGDVHWYQQLPQTAPKLLIYGN-----NRSGVDRPFGSK 87
2y 68 DEAHNACVLTISPVEDDADYYC 91
2b 88 --SGTSASLAITGLQAEDEADYYC 109

RESULT 9
ID OSWUK3 PRELIMINARY; PRT; 240 AA.
AC OSWUK3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RX TISSUE=Tonsil;
RM Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC020236; AAH20236.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;

Query Match 32.1%; Score 172.5; DB 4; Length 240;
Best Local Similarity 36.4%; Pred. No. 1.1e-11;
Matches 36; Conservative 20; Mismatches 30; Indels 13; Gaps 3;

2y 7 PQGVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAK 66
2b 32 FLGASIKLCTLSREH---SSVTIEWYQQRGSPQVIMKVKDGSNKGIDGIPDRFGMS 88
2y 67 KDAEHNACVLTISPVEDDADYYC-----SVGYGF 97
2b 89 SSGADR--YLTUSLQSDDEAEYHCGESHTTDGQVGWVF 125

RESULT 10
ID OSWUK3 PRELIMINARY; PRT; 240 AA.
AC OSWUK3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RX TISSUE=Tonsil;
RM Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC020236; AAH20236.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;

Query Match 32.1%; Score 172.5; DB 4; Length 240;
Best Local Similarity 36.4%; Pred. No. 1.1e-11;
Matches 36; Conservative 20; Mismatches 30; Indels 13; Gaps 3;

2y 7 PQGVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAK 66
2b 32 FLGASIKLCTLSREH---SSVTIEWYQQRGSPQVIMKVKDGSNKGIDGIPDRFGMS 88
2y 67 KDAEHNACVLTISPVEDDADYYC-----SVGYGF 97
2b 89 SSGADR--YLTUSLQSDDEAEYHCGESHTTDGQVGWVF 125

RESULT 11
ID OSWUK3 PRELIMINARY; PRT; 109 AA.
AC OSWUK3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Xu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,
RA Young D.C.;
RT fetus.;
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF03028; AAD56264.1; -.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 1
FT NON_TER 109 109

Query Match 31.4%; Score 169; DB 4; Length 107;
Best Local Similarity 41.7%; Pred. No. 1.1e-11;
Matches 35; Conservative 17; Mismatches 22; Indels 10; Gaps 3;

2y 9 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAK 68
2b 13 GQVTRITC-----QGSLSRYASWYQKPGQAPVLVIYK-----NNRPSGIPDRFSGS-- 62
2y 69 EAHNACVLTISPVEDDADYYCS 92
2b 63 SSGNTASLTITGAQAEDEADYYCN 86

RESULT 12
ID OSWUK3 PRELIMINARY; PRT; 109 AA.
AC OSWUK3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Xu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,
RA Young D.C.;
RT fetus.;
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF03028; AAD56264.1; -.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 1
FT NON_TER 109 109
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DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
KW SEQUENCE 234 AA; 24792 MW; CC848CAEB4A9D63 CRC64;
Query Match 29.9%; Score 161; DB 4; Length 234;
Best Local Similarity 40.9%; Pred. No. 2.2e-10;
Matches 36; Conservative 14; Mismatches 28; Indels 10; Gaps 3;
QY 6 VPPGVAQLSCTLSQHVITRDYGVSWYQORAGSAPRYLLYYRSEEDHHPADIPDRFSA 65
DB 31 VAPGQVARTICGNN-----NIGSKSVHWYQKQGPVLVYVY---DDSDRPSGIPERFSG 82
QY 66 AKDEAHNACVLTISPVPQEDDADYYCV 93
DB 83 S--NSGNTATLTISRVDAGDEADYYCQL 108
RESULT 14
Q99M11 PRELIMINARY; PRT; 235 AA.
ID Q99M11
AC Q99M11;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.4 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;
Query Match 29.9%; Score 161; DB 11; Length 235;
Best Local Similarity 42.2%; Pred. No. 2.2e-10;
Matches 35; Conservative 13; Mismatches 29; Indels 6; Gaps 2;
QY 9 GQVAQLSCTLSQHVITRDYGVSWYQORAGSAPRYLLYYRSEEDHHPADIPDRFSAKD 68
DB 34 GSTAKLPCKASTGN--ICDSYVNWYQQVMGRSPTMIY---GDDLRLPSGVSDRFGSID 87
QY 69 EAHNACVLTISPVPQEDDADYYC 91
DB 88 SSSNSAFLTIONVQADDEADYYC 110
RESULT 15
Q96SB0 PRELIMINARY; PRT; 108 AA.
ID Q96SB0
AC Q96SB0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin lambda light chain

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Search completed: February 9, 2004, 12:48:28
Job time : 31.2162 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

M protein - protein search, using sw model

run on: February 9, 2004, 08:36:32 ; Search time 30.7703 Seconds
(without alignments)
510.685 Million cell updates/sec

title: US-09-981-876-200_COPY_25_123

effect score: 538
sequence: 1 LDALLVFQVQAQLSCTLSP.....PVQEDDADYYCVSVGVGFSP 99

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Gapop 10.0 , Gapext 0.5

searched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters: 1107863

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database :

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 - 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
 - 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	100.0	113	22	AAW41476 Human polypeptide
2	538	100.0	123	19	AAW5123 Human secreted pro
3	538	100.0	123	21	AAW24061 Human PRO619 prote
4	538	100.0	123	21	AAW56655 Membrane-bound pro
5	538	100.0	123	22	AAU12372 Human PRO619 polyp
6	538	100.0	123	22	AAW65178 Human PRO619 (UNQ3
7	538	100.0	123	24	ABU65770 Human PRO polypept
8	538	100.0	123	24	ABU67046 Human secreted/tra
9	538	100.0	123	24	ABU59851 Novel secreted and

10	538	100.0	123	24	ABU59071 Novel human secret
11	538	100.0	123	24	ABU59218 Human secreted/tra
12	538	100.0	123	24	ABU59367 Novel human secret
13	538	100.0	123	24	ABU60502 Human secreted/tra
14	538	100.0	123	24	ABU57993 Human PRO polypept
15	538	100.0	123	24	ABU58924 Human secreted/tra
16	538	100.0	123	24	ABU58924 Human PRO619 polyp
17	538	100.0	123	24	ABU10839 Human PRO polypept
18	538	100.0	123	24	AAW39690 Human polypeptide
19	234.5	43.6	182	22	ABG19759 Novel human diagno
20	231.5	43.0	142	9	AAW83001 V preB-2 protein.
21	227.5	42.3	142	9	AAW80288 V preB-1 protein.
22	223.5	41.5	185	22	ABG29426 Novel human diagno
23	218.5	40.6	256	23	ABP45219 Human Blys binding
24	216.5	40.2	259	23	ABP45474 Human Blys binding
25	215.5	40.1	277	22	ABG19760 Novel human diagno
26	210.5	39.1	105	22	ABG22849 Novel human diagno
27	209.5	38.9	237	22	ABG19300 Novel human diagno
28	209.5	38.9	250	22	ABG19303 Novel human diagno
29	209.5	38.9	259	23	ABP45541 Human Blys binding
30	207.5	38.6	263	23	ABP45267 Human Blys binding
31	202	37.5	248	24	ABU19832 Human VEGF-2 relat
32	198	36.8	113	22	AAU02522 Anti-adipocyte mon
33	197	36.6	125	9	AAW80289 Human Vpre-B prote
34	195	36.2	98	24	ABP56510 Human anti-FC-epsi
35	195	36.2	134	13	AAW23771 Recombinant light
36	195	36.2	253	23	ABP44898 Human Blys binding
37	195	36.2	253	23	ABP45114 Human Blys binding
38	195	36.2	253	23	ABP45156 Human Blys binding
39	193	35.9	110	23	AAO18434 Anti-GD2 antibody
40	192.5	35.8	118	19	AAW57582 Chimeric H chain S
41	192.5	35.8	118	20	AAW89645 Human antibody hMB
42	192.5	35.8	118	21	AAW77506 Peptide seq ID No:
43	192.5	35.8	118	22	AAW63386 Amino acid sequenc
44	192.5	35.8	118	22	AAW64768 Humanised anti-PTH
45	192.5	35.8	118	22	AAW76884 Human antibody L C

ALIGNMENTS

RESULT 1
AAW41476
ID AAW41476 standard; Protein; 113 AA.
XX AAW41476;
AC AAW41476;
XX 22-OCT-2001 (first entry)
DT
DE Human polypeptide SEQ ID NO 6407.

Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX Homo sapiens.
XX
XX WO200153312-A1.
FN
XX 26-JUL-2001.
PD
XX 26-DEC-2000; 2000WO-US34263.
PF
XX 21-JAN-2000; 2000US-0488725.
PR
XX 25-APR-2000; 2000US-0552317.
PR
XX 09-JUL-2000; 2000US-0598042.
PR
XX 19-JUL-2000; 2000US-0620312.
PR
XX 03-AUG-2000; 2000US-0653450.
PR
XX 14-SEP-2000; 2000US-0662191.
PR
XX 19-OCT-2000; 2000US-0693036.

[illegible]

Query Match 100.0%; Score 538; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.4e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LDALLVFPQVQALSCITLSPQHVITRDYGVSWYQQRAGSAPRYLLYYRSEDDHRRADIP 60
25 LDALLVFPQVQALSCITLSPQHVITRDYGVSWYQQRAGSAPRYLLYYRSEDDHRRADIP 84

61 DRESAKOZAHNAACVLTISPVQFEDDADYICVGVGFSP 99
85 DRESAAKDEAHNAACVLTISPVQFEDDADYICVGVGFSP 123

RESULT 4

AY66655

ID AY66655 standard; protein; 123 AA.

CX AY66655;

CX

CX

CX 05-APR-2000 (first entry)

CX Membrane-bound protein PRO619.

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PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089807.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090576.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 11-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.

17-AUG-1998; 98US-0096891.
17-AUG-1998; 98US-0096894.
17-AUG-1998; 98US-0096895.
17-AUG-1998; 98US-0096897.
17-AUG-1998; 98US-0096899.
18-AUG-1998; 98US-0096949.
18-AUG-1998; 98US-0096950.
18-AUG-1998; 98US-0096959.
18-AUG-1998; 98US-0096960.
18-AUG-1998; 98US-0097022.
18-AUG-1998; 98US-0097141.
19-AUG-1998; 98US-0097218.
20-AUG-1998; 98US-0097661.
24-AUG-1998; 98US-0097661.
26-AUG-1998; 98US-0097951.
26-AUG-1998; 98US-0097952.
26-AUG-1998; 98US-0097954.
26-AUG-1998; 98US-0097955.
26-AUG-1998; 98US-0097971.
26-AUG-1998; 98US-0097974.
26-AUG-1998; 98US-0097978.
26-AUG-1998; 98US-0097979.
26-AUG-1998; 98US-0097986.
26-AUG-1998; 98US-0098014.
31-AUG-1998; 98US-0098525.
16-SEP-1998; 98US-0106834.
12-JAN-1999; 98US-0115565.
(GETH) GENENTECH INC.
Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
Wood WI, Yuan J;
WPI; 2000-072883/06.
N-PSDB; AAZ64983.
Membrane-bound proteins and related nucleotide sequences -
Claim 12; Fig 68; 822pp; English.
The invention provides membrane-bound PRO polypeptides and
polynucleotides encoding them. The PRO sequences of the invention were
identified based on extracellular domain homology screening. The PRO
sequences have homology with proteins including LDL receptors, TIE
ligands and various enzymes. The membrane-bound proteins and receptor
molecules are useful as pharmaceutical and diagnostic agents. Receptor
immunoadhesins, for instance, can be used as therapeutic agents to block
receptor-ligand interactions. The membrane-bound proteins can also be
employed for screening of potential peptide or small molecule inhibitors
of the relevant receptor/ligand interaction. The PRO encoding sequences
are useful as hybridization probes, in chromosome and gene mapping and in
the generation of antisense RNA and DNA. PRO nucleic acid sequences
will also be useful for the preparation of PRO polypeptides, especially
by recombinant techniques.
Query Match 100.0%; Score 539; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.4e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2Y 1 LDALLVFPQVQAQSLCSLSPQHVITRDYGVSWQVQAGSAPRYLLVYRSEEDHHPADIP 60
2b 25 LDALLVFPQVQAQSLCSLSPQHVITRDYGVSWQVQAGSAPRYLLVYRSEEDHHPADIP 84
2Y 61 DRFSAKDEAHNACVLITSPVQPEDDADYICSVGYGFSP 99
2b 85 DRFSAKDEAHNACVLITSPVQPEDDADYICSVGYGFSP 123
RESULT 5
AAU12372
ID AAU12372 standard; Protein; 123 AA.
XX
AC AAU12372;

XX 24-OCT-2001 (first entry)
DT Human PRO619 polypeptide sequence.
DE Human secretory and transmembrane; PRO; mammalian; cancer; lung;
XX breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX Homo sapiens.
OS WO200140466-A2.
XX 07-JUN-2001.
PD 01-DEC-2000; 200WO-US32678.
PF 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28554.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 200WO-US00277.
PR 06-JAN-2000; 200WO-US00376.
PR 11-FEB-2000; 200WO-US03565.
PR 18-FEB-2000; 200WO-US04341.
PR 18-FEB-2000; 200WO-US04342.
PR 22-FEB-2000; 200WO-US04414.
PR 24-FEB-2000; 200WO-US04914.
PR 24-FEB-2000; 200WO-US05004.
PR 01-MAR-2000; 200WO-US05601.
PR 20-MAR-2000; 200WO-US07377.
PR 21-MAR-2000; 200WO-US07532.
PR 30-MAR-2000; 200WO-US08439.
PR 17-MAY-2000; 200WO-US13705.
PR 22-MAY-2000; 200WO-US14042.
PR 30-MAY-2000; 200WO-US14941.
PR 02-JUN-2000; 200WO-US15264.
PR 10-NOV-2000; 200WO-US30873.
(GETH) GENENTECH INC.
Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen WB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2001-408281/43.
N-PSDB; AAS21444.
Isolated, secretory and transmembrane PRO polypeptide used to detect
other PRO polypeptides, link bioactive molecules to cells expressing
PRO polypeptides, and detect the presence of mammalian tumours e.g.
lung, breast, prostate, cervical
Claim 12; Fig 402; 813pp; English.
AAU12172-AAU12446 represent novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bioactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from

C cartilage, the proliferation of inner ear utricular supporting cells or
C of T-lymphocytes, the release of a cytokine from peripheral blood
C monocytes (PBMCs), or the proliferation of endothelial cells. Some of
C the PRO polypeptides may modulate glucose or free fatty acid uptake by
C skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
C to factor VIIa. The PRO polypeptides can be used in assays to identify
C molecules involved in binding interactions. The polynucleotides encoding
C PRO polypeptides can be used to generate probes, antisense RNA/DNA,
C transgenic or knock out animals and can be used in gene therapy.
X
Q

Sequence 123 AA;
Query Match 100.0%; Score 538; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.4e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LDALLVPPGVAQLSCTLSFQVHTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIP 60
25 LDALLVPPGVAQLSCTLSFQVHTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIP 84
61 DRFSAKDEAHNACVLTISFPQEDDADYICSVGVGFSP 99
85 DRFSAKDEAHNACVLTISFPQEDDADYICSVGVGFSP 123

RESULT 6
AAB65178
ID AAB65178 standard; Protein; 123 AA.
AC AAB65178;
XX

02-APR-2001 (first entry)
XX Human PRO619 (UNQ355) protein sequence SEQ ID NO:117.
DE Human; secreted and transmembrane protein; PRO; cytostatic;
XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX Homo sapiens.
XX WO2000073454-A1.
XX 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US08439.
XX
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 17-AUG-1999; 99US-0149396.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 08-OCT-1999; 99US-0158663.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28301.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 02-MAR-2000; 2000WO-US05841.
XX 15-MAR-2000; 2000WO-US06884.
XX 20-MAR-2000; 2000WO-US07377.
XX (GETH) GENENTECH INC.
PA

XX Ashkenazi AJ, Baker KP, Botstein D, Desnuyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski BJ;
PI Grimaldi CJ, Gurney AL, Klijavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy NA, Stewart TA, Tumas D, Watanabe CK, Williams EM, Wood WI;
PI Zhang Z;
XX WPI; 2001-032160/04.
DR N-PSDB; AAF44129.
XX

PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
PS Claim 12; Fig 68; 935pp; English.
XX

The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.4e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDALLVPPGVAQLSCTLSFQVHTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIP 60
DB 25 LDALLVPPGVAQLSCTLSFQVHTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIP 84
QY 61 DRFSAKDEAHNACVLTISFPQEDDADYICSVGVGFSP 99
DB 85 DRFSAKDEAHNACVLTISFPQEDDADYICSVGVGFSP 123

RESULT 7
AAB65178
ID AAB65178 standard; Protein; 123 AA.
XX
AC AAB65178;
XX
XX 23-MAY-2003 (first entry)
XX Human PRO polypeptide #201.
XX Human; PRO polypeptide; secreted and transmembrane protein;
XX tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
XX differentiation; chondrocyte; tumour; genetic disorder;
XX cytostatic.
XX Homo sapiens.
XX US2003036180-A1.
XX
XX 20-FEB-2003.
XX
XX 09-MAY-2002; 2002US-0143114.
XX
XX 31-MAR-1997; 97WO-US05230.
XX 12-JUN-1998; 98WO-US12456.
XX 14-JUL-1998; 98WO-US14552.
XX 28-AUG-1998; 98WO-US17888.

RESULT 8

BU67046

D ABU67046 standard; Protein; 123 AA.

X C ABU67046;

X T 27-MAY-2003 (first entry)

X E Human secreted/transmembrane, PRO, protein SEQ ID 402.

X W Human; secreted protein; transmembrane protein; PRO;
X W inflammatory disease; organ failure; atherosclerosis; cardiac injury;
X W infertility; birth defects; premature aging; AIDS; biosensor;
X W acquired immunodeficiency syndrome; cancer; diabetic complication;
X W bioreactor; tumour.

X S Homo sapiens.

X N US2003032155-A1.

X D 13-FEB-2003.

X F 03-MAY-2002; 2002US-0137865.

X C 31-MAR-1997; 97WO-US05230.

X R 12-JUN-1998; 98WO-US12456.

X R 14-JUL-1998; 98WO-US14552.

X R 28-AUG-1998; 98WO-US17888.

X R 10-SEP-1998; 98WO-US18824.

X R 14-SEP-1998; 98WO-US19093.

X R 14-SEP-1998; 98WO-US19094.

X R 16-SEP-1998; 98WO-US19177.

X R 17-SEP-1998; 98WO-US19330.

X R 07-OCT-1998; 98WO-US19437.

X R 29-OCT-1998; 98WO-US22991.

X R 29-OCT-1998; 98WO-US22992.

X R 01-DEC-1998; 98WO-US24855.

X R 05-JAN-1999; 99WO-US00106.

X R 08-MAR-1999; 99WO-US05028.

X R 10-MAR-1999; 99WO-US05190.

X R 20-APR-1999; 99WO-US08615.

X R 14-MAY-1999; 99WO-US10733.

X R 02-JUN-1999; 99WO-US12252.

X R 01-SEP-1999; 99WO-US20111.

X R 08-SEP-1999; 99WO-US20594.

X R 13-SEP-1999; 99WO-US20944.

X R 15-SEP-1999; 99WO-US21090.

X R 05-OCT-1999; 99WO-US21547.

X R 29-NOV-1999; 99WO-US23089.

X R 30-NOV-1999; 99WO-US28214.

X R 30-NOV-1999; 99WO-US28313.

X R 01-DEC-1999; 99WO-US28409.

X R 01-DEC-1999; 99WO-US28301.

X R 01-DEC-1999; 99WO-US28634.

X R 02-DEC-1999; 99WO-US28551.

X R 02-DEC-1999; 99WO-US28564.

X R 16-DEC-1999; 99WO-US30095.

X R 20-DEC-1999; 99WO-US30911.

X R 20-DEC-1999; 99WO-US30999.

X R 22-DEC-1999; 99WO-US30720.

X R 30-DEC-1999; 99WO-US31243.

X R 05-JAN-2000; 99WO-US31274.

X R 06-JAN-2000; 2000WO-US00219.

X R 11-FEB-2000; 2000WO-US00376.

X R 18-FEB-2000; 2000WO-US03565.

X R 22-FEB-2000; 2000WO-US04341.

X R 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 03-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0860216.
PR 01-JUN-2001; 2001US-0866034.
PR 05-JUN-2001; 2001US-0872035.
PR 14-JUN-2001; 2001US-0874503.
PR 19-JUN-2001; 2001US-0882636.
PR 21-JUN-2001; 2001US-0886342.
PR 18-JUL-2001; 2001US-0887879.
PR 21-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2003-331925/31.

N-PSDB; ACA04224.

New secreted and transmembrane nucleic acids and polypeptides,
designated as PRO, useful for treating inflammation, organ failure,
atherosclerosis, cardiac injury, infertility, birth defects, premature
aging, AIDS, or cancer

Claim 12; Fig 402; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is
at least 80% identical to, or the full-length coding sequence of, any of
the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
(one of 275 secreted or transmembrane proteins). The nucleic acid
further comprises the full-length coding sequence of the DNA deposited

C under American Type Culture Collection (ATCC) accession number in a list
 C given in the specification. Also included are vectors and host
 C cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 C antibodies, PRO extracellular domains and mature sequences, methods
 C of detecting PRO proteins, methods for stimulating the release of
 C TNF-alpha (tumour necrosis factor alpha) from human blood,
 C (and the proliferation of differentiation of chondrocyte cells, the
 C proliferation of, or gene expression in pericyte cells, the release or
 C proteoglycans from cartilage, proliferation of inner ear utricular
 C supporting cells, the proliferation of T-lymphocyte cells, the release
 C of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 C proliferation of endothelial cells), a method for modulating the uptake
 C of glucose or free fatty acid (FFA) by skeletal muscle cells,
 C a method for inhibiting the binding of A-peptide to factor VIIa,
 C or the differentiation of adipocyte cells, a method for detecting the
 C presence of a tumour in a mammal and an oligonucleotide probe derived
 C from any of the nucleotide sequences cited above. The nucleic acids and
 C polypeptides are useful for treating inflammatory diseases, organ
 C failure, atherosclerosis, cardiac injury, infertility, birth defects,
 C premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 C diabetic complications. The nucleic acids are useful as hybridisation
 C probes, in chromosome and gene mapping, and in generating antisense RNA
 C or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 C biosensors or bioreactors. Both are useful in tissue typing.
 C The present sequence represents a PRO protein of the invention.

X Sequence 123 AA;

Query Match 100.0%; Score 538; DB 24; Length 123;
 Best Local Similarity 100.0%; Pred. No. 7.4e-53;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 LDALLVPPGVAQLSCTLSQFQVTRDYGVSVYQQRAGSAPRYLLYRSEEDHRRPADIP 60

b 25 LDALLVPPGVAQLSCTLSQFQVTRDYGVSVYQQRAGSAPRYLLYRSEEDHRRPADIP 84

Y 61 DRFSAKDEAHNAVLITISFQVEDDADYICSVGYGFSP 99

b 85 DRFSAKDEAHNAVLITISFQVEDDADYICSVGYGFSP 123

RESULT 9

BU59851

D ABUS9851 standard; Protein; 123 AA.

X C ABUS9851;

X 13-MAY-2003 (first entry)

X Novel secreted and transmembrane protein PRO619.

X Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 X cardiac insufficiency disorder; cancer; tumour; immune response;
 X adrenal cortical capillary endothelial growth; c-fos induction;
 X vascular endothelial growth factor inhibition; VEGF inhibition;
 X endothelial cell growth inhibitor; T-lymphocytes stimulation;
 X retinal neurons cell survival; rod photoreceptor cell survival;
 X retinal disorder; retinitis pigmentosa; kidney disorder;
 X mammalian kidney mesangial cell proliferation; Berger disease;
 X dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 X chondrocyte redifferentiation; sports injury; arthritis.

X Homo sapiens.

X US2003017563-A1.

X 23-JAN-2003.

X 07-MAY-2002; 2002US-0140808.

X 31-MAR-1997; 97WO-US05230.

X 12-JUN-1998; 98WO-US12456.

X 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 16-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 98WO-US00106.
 PR 08-MAR-1999; 98WO-US05028.
 PR 10-MAR-1999; 98WO-US05190.
 PR 20-APR-1999; 98WO-US08615.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20594.
 PR 13-SEP-1999; 98WO-US20944.
 PR 15-SEP-1999; 98WO-US21090.
 PR 15-SEP-1999; 98WO-US21547.
 PR 05-OCT-1999; 98WO-US23089.
 PR 29-NOV-1999; 98WO-US28214.
 PR 30-NOV-1999; 98WO-US28313.
 PR 30-NOV-1999; 98WO-US28409.
 PR 01-DEC-1999; 98WO-US28301.
 PR 01-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 02-DEC-1999; 98WO-US28564.
 PR 02-DEC-1999; 98WO-US28565.
 PR 16-DEC-1999; 98WO-US30095.
 PR 20-DEC-1999; 98WO-US30911.
 PR 20-DEC-1999; 98WO-US30999.
 PR 22-DEC-1999; 98WO-US30720.
 PR 30-DEC-1999; 98WO-US31243.
 PR 30-DEC-1999; 98WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 23-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US33678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.

R 29-JUN-2001; 2001WO-US21066.
R 09-JUL-2001; 2001WO-US21735.
R 20-DEC-2000; 2000US-0747259.
R 28-FEB-2001; 2001US-0796498.
R 09-MAR-2001; 2001US-0802706.
R 14-MAR-2001; 2001US-0808689.
R 22-MAR-2001; 2001US-0816744.
R 05-APR-2001; 2001US-0828366.
R 10-MAY-2001; 2001US-0854208.
R 18-MAY-2001; 2001US-0854280.
R 23-MAY-2001; 2001US-0860216.
R 25-MAY-2001; 2001US-0866028.
R 25-MAY-2001; 2001US-0866034.
R 01-JUN-2001; 2001US-0872035.
R 05-JUN-2001; 2001US-0874503.
R 14-JUN-2001; 2001US-0882636.
R 19-JUN-2001; 2001US-0886342.
R 21-JUN-2001; 2001US-0887879.
R 18-JUL-2001; 2001US-0908827.
R 06-AUG-2001; 2001US-0924419.
R 09-AUG-2001; 2001US-0927796.
R 16-AUG-2001; 2001US-0931836.
R 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-148238/14.
DR N-PSDB; ABX89341.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -

XX Claim 12; Fig 402; 659pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1134 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1132 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC is the amino acid sequence of a novel human PRO protein.

XX Sequence 123 AA;

XX Query Match 100.0%; Score 538; DB 24; Length 123;

Best Local Similarity 100.0%; Pred. No. 7 4e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEDDHRRADIP 60
Db 25 LDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEDDHRRADIP 84
Qy 61 DRFSAKDEAHNACVLTISPVPQEDDADYICVGVGFSP 99
Db 85 DRFSAKDEAHNACVLTISPVPQEDDADYICVGVGFSP 123

RESULT 10

ABUS9071

ID ABUS9071 standard; Protein; 123 AA.

XX AC ABUS9071;

XX DT 28-APR-2003 (first entry)

XX DE Novel human secreted or transmembrane protein PRO619.

XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;

XX KW cardiac insufficiency disorder; cancer; tumour; immune response;

XX KW adrenal cortical capillary endothelial growth; c-fos induction;

XX KW vascular endothelial growth factor inhibition; VEGF inhibition;

XX KW endothelial cell growth inhibitor; T-lymphocytes stimulation;

XX KW retinal neurons cell survival; rod photoreceptor cell survival;

XX KW retinal disorder; retinitis pigmentosa; kidney disease;

XX KW mammalian kidney mesangial cell proliferation; Berger disease;

XX KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;

XX KW chondrocyte redifferentiation; sports injury; arthritis.

XX OS Homo sapiens.

XX US20002132252-A1.

XX PD 19-SEP-2002.

XX PF 14-NOV-2001; 2001US-0990442.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 16-DEC-1999; 99WO-US28634.

XX PR 20-DEC-1999; 99WO-US30095.

XX PR 06-JAN-2000; 2000WO-US00911.

XX PR 06-JAN-2000; 2000WO-US00219.

XX PR 11-FEB-2000; 2000WO-US03565.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 22-FEB-2000; 2000WO-US04414.

XX PR 24-FEB-2000; 2000WO-US04914.

XX PR 02-MAR-2000; 2000WO-US05004.

XX PR 10-MAR-2000; 2000WO-US05841.

XX PR 15-MAR-2000; 2000WO-US06319.

XX PR 20-MAR-2000; 2000WO-US06884.

XX PR 30-MAR-2000; 2000WO-US07377.

XX PR 15-MAY-2000; 2000WO-US13358.

XX PR 17-MAY-2000; 2000WO-US13705.

XX PR 22-MAY-2000; 2000WO-US14042.

XX PR 30-MAY-2000; 2000WO-US14941.

XX PR 02-JUN-2000; 2000WO-US15264.

R 28-JUL-2000; 2000WO-US20710.
R 11-AUG-2000; 2000WO-US22031.
R 23-AUG-2000; 2000WO-US23522.
R 24-AUG-2000; 2000WO-US23328.
R 08-NOV-2000; 2000WO-US30952.
R 01-DEC-2000; 2000WO-US32678.
R 28-FEB-2001; 2001WO-US06520.
R 01-JUN-2001; 2001WO-US17800.
R 20-JUN-2001; 2001WO-US19692.
R 29-JUN-2001; 2001WO-US21066.
R 09-JUL-2001; 2001WO-US21735.
R 16-JUN-1997; 97US-049787P.
R 17-OCT-1997; 97US-062250P.
R 12-NOV-1997; 97US-065186P.
R 13-NOV-1997; 97US-065311P.
R 24-NOV-1997; 97US-066770P.
R 25-FEB-1998; 98US-075945P.
R 20-MAR-1998; 98US-078910P.
R 28-APR-1998; 98US-083322P.
R 07-MAY-1998; 98US-084600P.
R 28-MAY-1998; 98US-087106P.
R 02-JUN-1998; 98US-087607P.
R 02-JUN-1998; 98US-087609P.
R 02-JUN-1998; 98US-087759P.
R 03-JUN-1998; 98US-087827P.
R 04-JUN-1998; 98US-088021P.
R 04-JUN-1998; 98US-088025P.
R 04-JUN-1998; 98US-088026P.
R 04-JUN-1998; 98US-088028P.
R 04-JUN-1998; 98US-088029P.
R 04-JUN-1998; 98US-088030P.
R 04-JUN-1998; 98US-088033P.
R 04-JUN-1998; 98US-088326P.
R 05-JUN-1998; 98US-088167P.
R 05-JUN-1998; 98US-088202P.
R 05-JUN-1998; 98US-088212P.
R 05-JUN-1998; 98US-088217P.
R 09-JUN-1998; 98US-088655P.
R 10-JUN-1998; 98US-088734P.
R 10-JUN-1998; 98US-088738P.
R 10-JUN-1998; 98US-088742P.
R 10-JUN-1998; 98US-088810P.
R 10-JUN-1998; 98US-088824P.
R 11-JUN-1998; 98US-088826P.
R 11-JUN-1998; 98US-088858P.
R 11-JUN-1998; 98US-088861P.
R 11-JUN-1998; 98US-088876P.
R 12-JUN-1998; 98US-089105P.
R 16-JUN-1998; 98US-089440P.
R 16-JUN-1998; 98US-089512P.
R 16-JUN-1998; 98US-089514P.
R 17-JUN-1998; 98US-089532P.
R 17-JUN-1998; 98US-089538P.
R 17-JUN-1998; 98US-089598P.
R 17-JUN-1998; 98US-089599P.
R 17-JUN-1998; 98US-089600P.
R 17-JUN-1998; 98US-089653P.
R 18-JUN-1998; 98US-089801P.
R 18-JUN-1998; 98US-089907P.
R 28-JUN-1998; 98US-089908P.
R 28-AUG-2001; 2001US-094192.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;

XX WPI; 2003-247083/24.
DR N-PSDB; ABX80196.
XX

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments
XX
PS Claim 12; Fig 68; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonism of this polypeptide are
CC useful for treating cancerous tumours. PRO12 inhibits vascular
CC endothelial growth factor (VEGF) stimulated endothelial cell growth in
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, and PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1068 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or Crohn's
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC is the amino acid sequence of a novel human PRO protein.
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.4e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDALLVFPQVVAQLSCTLSPPQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHRRADIP 60
DB 25 LDALLVFPQVVAQLSCTLSPPQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHRRADIP 84
QY 61 DRFSAKDEAHNACVLTISPQVEDDADYVCVGYGFSP 99
DB 85 DRFSAKDEAHNACVLTISPQVEDDADYVCVGYGFSP 123

RESULT 11

ABU59218
ID ABU59218 standard; Protein; 123 AA.

XX AC ABU59218;

XX 22-APR-2003 (first entry)

XX Human secreted/transmembrane protein, #43.

XX Human; PRO; secreted; transmembrane; pharmaceutical;
XX diagnostic; biosensor; bioreactor; tumour; therapeutic;
XX Gene therapy; tumour-associated antigenic target; TAT; ADEPT;
XX antibody-dependent enzyme mediated prodrug therapy; cytostatic.

XX Homo sapiens.

XX OS

XX US2003027162-A1.

XX 06-FEB-2003.

XX

IF 15-NOV-2001; 2001US-0997428.
XX 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 02-MAR-2000; 2000WO-US05004.
PR 10-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06319.
PR 20-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US07377.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30352.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062250P.
PR 12-NOV-1997; 97US-065186P.
PR 13-NOV-1997; 97US-065311P.
PR 25-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 28-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
PR 02-JUN-1998; 98US-087607P.
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PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088021P.
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PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 24-JUN-1998; 98US-090542P.
PR 24-JUN-1998; 98US-090557P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
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PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 01-JUL-1998; 98US-091360P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091519P.
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PR 02-JUL-1998; 98US-091633P.
PR 02-JUL-1998; 98US-091646P.
PR 02-JUL-1998; 98US-091673P.
PR 07-JUL-1998; 98US-091978P.
PR 07-JUL-1998; 98US-091982P.
PR 09-JUL-1998; 98US-092182P.
PR 10-JUL-1998; 98US-092472P.
PR 20-JUL-1998; 98US-093339P.
PR 30-JUL-1998; 98US-094651P.
PR 04-AUG-1998; 98US-095282P.
PR 04-AUG-1998; 98US-095285P.
PR 04-AUG-1998; 98US-095301P.
PR 04-AUG-1998; 98US-095302P.
PR 04-AUG-1998; 98US-095318P.
PR 04-AUG-1998; 98US-095321P.
PR 04-AUG-1998; 98US-095325P.
PR 10-AUG-1998; 98US-095916P.
PR 10-AUG-1998; 98US-095929P.
PR 10-AUG-1998; 98US-096012P.
PR 11-AUG-1998; 98US-096143P.

R 11-AUG-1998; 98US-096146P.
R 12-AUG-1998; 98US-096329P.
R 17-AUG-1998; 98US-096757P.
R 17-AUG-1998; 98US-096766P.
R 17-AUG-1998; 98US-096768P.
R 17-AUG-1998; 98US-096773P.
R 17-AUG-1998; 98US-096791P.
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R 17-AUG-1998; 98US-096894P.
R 17-AUG-1998; 98US-096895P.
R 17-AUG-1998; 98US-096897P.
R 18-AUG-1998; 98US-096949P.
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R 18-AUG-1998; 98US-096960P.
R 18-AUG-1998; 98US-097022P.
R 19-AUG-1998; 98US-097141P.
R 20-AUG-1998; 98US-097218P.
R 24-AUG-1998; 98US-097661P.
R 26-AUG-1998; 98US-097952P.
R 26-AUG-1998; 98US-097954P.
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R 26-AUG-1998; 98US-097978P.
R 26-AUG-1998; 98US-097979P.
R 26-AUG-1998; 98US-097986P.
R 26-AUG-1998; 98US-098014P.
R 31-AUG-1998; 98US-098525P.
R 16-SEP-1998; 98US-100634P.
R 17-SEP-1998; 98US-100858P.
R 22-DEC-1998; 98US-113296P.
R 12-MAR-1999; 99US-123957P.
R 23-JUN-1999; 99US-141037P.

Query Match 100.0%; Score 538; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.4e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LDALLVPPGVAQLSCTLSPOHTIYDYGVSWMYQOAGSAPRYLLYYSEEDHHPADIP 60
25 LDALLVPPGVAQLSCTLSPOHTIYDYGVSWMYQOAGSAPRYLLYYSEEDHHPADIP 84

61 DRFSAKDEAHNAACVLITSPVQPEDDADYCYSGYGFSP 99
85 DRFSAKDEAHNAACVLITSPVQPEDDADYCYSGYGFSP 123

RESULT 12
ABUS9367
ID ABUS9367 standard; Protein; 123 AA.
AC ABUS9367;
CX
CX 22-APR-2003 (first entry)
CX
CX Novel human secreted or transmembrane protein PRO943.
CX
CX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
CX Cardiac insufficiency disorder; cancer; tumour; immune response;
CX adrenal cortical capillary endothelial growth; c-fos induction;
CX vascular endothelial growth factor inhibition; VEGF inhibition;
CX endothelial cell growth inhibitor; T-lymphocytes stimulation;
CX retinal neurons cell survival; rod photoreceptor cell survival;
CX retinal disorder; retinitis pigmentosa; kidney disease;
CX mammalian kidney mesangial cell proliferation; Berger disease;
CX dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
CX chondrocyte redifferentiation; sports injury; arthritis.
CX
CX Homo sapiens.
OS
XX
XX US2003027985-A1.
PN

XX PD
XX PF
XX
XX
PR 06-FEB-2003.
PR 14-NOV-2001; 2001US-0990562.
PR 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062250P.
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Best Local Similarity 100.0%; Pred. No. 7.4e-53;

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DB 25 LDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHRRPADIP 84

QY 61 DRFSAKDEAHNACVLTISPVQPEDDADYICSVGVGFSP 99

DB 85 DRFSAKDEAHNACVLTISPVQPEDDADYICSVGVGFSP 123

RESULT 13

ABU60502

ID ABU60502 standard; Protein; 123 AA.

XX AC ABU60502;

XX DT 01-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein, #43.

XX KW Human; PRO; secreted; transmembrane; signal peptide;

XX KW pharmaceutical; diagnostic; therapeutic; gene therapy.

XX OS Homo sapiens.

XX FN US20002160384-A1.

XX PD 31-OCT-2002.

XX PF 14-NOV-2001; 2001US-0992598.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 16-SEP-1988; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

3 08-MAR-1999; 99WO-US05028.
 4 02-JUN-1999; 99WO-US12252.
 5 15-SEP-1999; 99WO-US21090.
 6 15-SEP-1999; 99WO-US21547.
 7 30-NOV-1999; 99WO-US28313.
 8 01-DEC-1999; 99WO-US28301.
 9 01-DEC-1999; 99WO-US28634.
 10 16-DEC-1999; 99WO-US30095.
 11 20-DEC-1999; 99WO-US30911.
 12 05-JAN-2000; 2000WO-US00219.
 13 06-JAN-2000; 2000WO-US00376.
 14 11-FEB-2000; 2000WO-US03565.
 15 18-FEB-2000; 2000WO-US04341.
 16 22-FEB-2000; 2000WO-US04414.
 17 24-FEB-2000; 2000WO-US04914.
 18 24-FEB-2000; 2000WO-US05004.
 19 10-MAR-2000; 2000WO-US05841.
 20 15-MAR-2000; 2000WO-US06319.
 21 20-MAR-2000; 2000WO-US06884.
 22 30-MAR-2000; 2000WO-US07377.
 23 15-MAY-2000; 2000WO-US08439.
 24 17-MAY-2000; 2000WO-US13358.
 25 22-MAY-2000; 2000WO-US13705.
 26 30-MAY-2000; 2000WO-US14042.
 27 02-JUN-2000; 2000WO-US14941.
 28 02-JUN-2000; 2000WO-US15264.
 29 28-JUL-2000; 2000WO-US20710.
 30 11-AUG-2000; 2000WO-US22031.
 31 23-AUG-2000; 2000WO-US23522.
 32 24-AUG-2000; 2000WO-US23328.
 33 08-NOV-2000; 2000WO-US30952.
 34 01-DEC-2000; 2000WO-US32678.
 35 28-FEB-2001; 2001WO-US06520.
 36 01-JUN-2001; 2001WO-US17800.
 37 29-JUN-2001; 2001WO-US19692.
 38 09-JUL-2001; 2001WO-US21735.
 39 16-JUN-1997; 97US-049787P.
 40 17-OCT-1997; 97US-062250P.
 41 12-NOV-1997; 97US-065186P.
 42 13-NOV-1997; 97US-065311P.
 43 24-NOV-1997; 97US-068770P.
 44 25-FEB-1998; 98US-075945P.
 45 20-MAR-1998; 98US-078910P.
 46 28-APR-1998; 98US-083322P.
 47 07-MAY-1998; 98US-084600P.
 48 02-JUN-1998; 98US-087106P.
 49 02-JUN-1998; 98US-087607P.
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 66 10-JUN-1998; 98US-088734P.
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 74 11-JUN-1998; 98US-088876P.

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 PR 17-JUN-1998; 98US-089653P.
 PR 18-JUN-1998; 98US-089801P.
 PR 18-JUN-1998; 98US-089807P.
 PR 18-JUN-1998; 98US-089908P.
 PR 28-AUG-2001; 2001US-0941992.

(GETH) GENENTECH INC.

Aehkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 Zhang Z;

WPI: 2003-288106/28.
 N-PSDB; ABX90174.

New transmembrane polypeptides and nucleic acids encoding the
 polypeptides, useful in gene therapy, in chromosome identification, as
 chromosome markers, or in generating probes -

Claim 12; Fig 68; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides
 comprising a sequence without signal peptide and the nucleic acid
 encoding them. The polypeptides can be used to raise antibodies that
 specifically bind to the PRO polypeptide, for linking a bioactive
 molecule to a cell expressing a PRO protein and for modulating at least
 one biological activity of a cell. The PRO polypeptides or
 polynucleotides are also useful in gene therapy, in chromosome
 identification, as chromosome markers, or in generating probes. The PRO
 polypeptides are useful as molecular markers for protein
 electrophoresis, and the isolated nucleic acids may be used for
 recombinantly expressing those markers. The PRO polypeptides and nucleic
 acids may also be used in tissue typing. Anti-PRO antibodies are useful
 in diagnostic assays for PRO, and in affinity purification of PRO from
 recombinant cell culture or natural sources. The sequences presented in
 CC ABU60478-ABU60624 are the PRO polynucleotides of the invention.
 CC Note: The sequence data for this patent is also available in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 24; Length 123;
 Best Local Similarity 100.0%; Pred. No. 7.4e-53;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDALLVFGQVAQLSCTLSPOHVTIRYGVSWQORAGSAPRYLLYRSEEDHRRADIP 60
 DB 25 LDALLVFGQVAQLSCTLSPOHVTIRYGVSWQORAGSAPRYLLYRSEEDHRRADIP 84
 QY 61 DRFSAKDEAHNACVLTISPVQPEDDADYTCVGYGFSP 99
 DB 85 DRFSAKDEAHNACVLTISPVQPEDDADYTCVGYGFSP 123

RESULT 14

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 AC ABUS7993;
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 DT 14-APR-2003 (first entry)
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Human PRO polypeptide #25.
Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
Homo sapiens.
US2003027163-A1.
06-FEB-2003.
15-NOV-2001; 2001US-0997666.
05-NOV-1997; 97WO-US20069.
16-SEP-1998; 98WO-US19330.
17-SEP-1998; 98WO-US19437.
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05-JAN-1999; 99WO-US00106.
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15-SEP-1999; 99WO-US21547.
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20-DEC-1999; 99WO-US30911.
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24-AUG-2000; 2000WO-US23328.
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07-JUL-1998; 98US-091978P.
07-JUL-1998; 98US-091982P.
09-JUL-1998; 98US-092182P.
10-JUL-1998; 98US-092472P.
20-JUL-1998; 98US-093339P.

pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
colon cancer; lung cancer; breast cancer; cancer; gene therapy.

Homo sapiens.

US2002142961-A1.

03-OCT-2002.

19-NOV-2001; 2001US-0989721.

05-NOV-1997; 97WO-US20069.

17-SEP-1998; 98WO-US19437.

07-OCT-1998; 98WO-US21141.

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08-MAR-1999; 99WO-US05028.

02-JUN-1999; 99WO-US12252.

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PR 05-DEC-1999; 99WO-US30911.

PR 20-JAN-2000; 2000WO-US00219.

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PR 11-FEB-2000; 2000WO-US03565.

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PR 02-MAR-2000; 2000WO-US05004.

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PR 10-MAR-2000; 2000WO-US06319.

PR 15-MAR-2000; 2000WO-US06884.

PR 30-MAR-2000; 2000WO-US08439.

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PR 08-NOV-2000; 2000WO-US30952.

PR 01-DEC-2000; 2000WO-US33678.

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XX	PR	24-NOV-1997; 97US-066770P.
XX	PR	25-FEB-1998; 98US-075945P.
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XX	PR	02-JUN-1998; 98US-087759P.
XX	PR	03-JUN-1998; 98US-087827P.
XX	PR	04-JUN-1998; 98US-088021P.
XX	PR	04-JUN-1998; 98US-088025P.
XX	PR	04-JUN-1998; 98US-088026P.
XX	PR	04-JUN-1998; 98US-088028P.
XX	PR	04-JUN-1998; 98US-088029P.
XX	PR	04-JUN-1998; 98US-088030P.

Query Match		100.0%; Score 538; DB 24; Length 123;
Best Local Similarity		100.0%; Pred. No. 7.4e-53;
Matches 99; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
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2b	25	LDALLVPGQVAQLSCTLSQHVITRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84
2Y	61	DRFSAKDEAHNACVLITSPQPEDDADYICSVGYGFSP 99
2b	85	DRFSAKDEAHNACVLITSPQPEDDADYICSVGYGFSP 123

RESULT 15
ABUS8924
ID ABUS8924 standard; Protein, 123 AA.
XX AC ABUS8924;
XX DT 16-APR-2003 (first entry)
XX DE Human secreted/transmembrane protein, #43.
XX KW Human; PRO; secreted; transmembrane; signal peptide;

PR 04-JUN-1998; 98US-088033P.

PR 04-JUN-1998; 98US-088326P.

PR 05-JUN-1998; 98US-088167P.

PR 05-JUN-1998; 98US-088202P.

PR 05-JUN-1998; 98US-088212P.

PR 05-JUN-1998; 98US-088217P.

PR 09-JUN-1998; 98US-088655P.

PR 10-JUN-1998; 98US-088734P.

PR 10-JUN-1998; 98US-088738P.

PR 10-JUN-1998; 98US-088742P.

PR 10-JUN-1998; 98US-088810P.

PR 10-JUN-1998; 98US-088824P.

PR 10-JUN-1998; 98US-088826P.

PR 11-JUN-1998; 98US-088859P.

PR 11-JUN-1998; 98US-088861P.

PR 11-JUN-1998; 98US-088876P.

PR 12-JUN-1998; 98US-089105P.

PR 16-JUN-1998; 98US-089440P.

PR 16-JUN-1998; 98US-089512P.

PR 16-JUN-1998; 98US-089514P.

PR 17-JUN-1998; 98US-089532P.

PR 17-JUN-1998; 98US-089538P.

PR 17-JUN-1998; 98US-089598P.

PR 17-JUN-1998; 98US-089599P.

PR 17-JUN-1998; 98US-089600P.

PR 17-JUN-1998; 98US-089653P.

PR 18-JUN-1998; 98US-089801P.

PR 18-JUN-1998; 98US-089907P.

PR 18-JUN-1998; 98US-089908P.

PR 28-AUG-2001; 2001US-094199P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

XX Zhang Z;

XX WPI; 2003-155950/15.

XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers

XX Claim 12; Fig 68; 647pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers). The PRO polypeptides are also useful as presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ASU58900-ABU59046 are the PRO polypeptides of the invention.

XX Sequence 123 AA;

XX Query Match 100.0%; Score 538; DB 24; Length 123;

XX Best Local Similarity 100.0%; Pred. No. 7.4e-53;

XX Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDALLVFFGQVAQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60

Db 25 LDALLVFFGQVAQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

QY 61 DRFSAAKDEAHNACVLTISPVQPEDDADYICSVGYGFSF 99

Db 85 DRFSAAKDEAHNACVLTISPVQPEDDADYICSVGYGFSF 123

Search completed: February 9, 2004, 12:45:53

Job time : 32.7703 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: February 9, 2004, 12:47:07 ; Search time 28.9865 seconds
(without alignments)
715.121 Million cell updates/sec

File:
Perfect score: 538
Sequence: 1 LDALLVPCQVAQLSCTLSF.....PVQPEDDADYCVSVGYGFSP 99

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues 801455

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp:*
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ALIGNMENTS

RESULT 1

US-09-989-722-117

Sequence 117, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides, and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C63

CURRENT APPLICATION NUMBER: US/09/989, 722

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	538	100.0	123	9	US-09-989-722-117
2	538	100.0	123	9	US-09-989-723-117
3	538	100.0	123	9	US-09-989-279-117
4	538	100.0	123	9	US-09-989-727-117
5	538	100.0	123	9	US-09-989-731-117
6	538	100.0	123	10	US-09-989-732-117
7	538	100.0	123	10	US-09-991-073-117
8	538	100.0	123	10	US-09-990-442-117
9	538	100.0	123	10	US-09-991-163-117
10	538	100.0	123	10	US-09-993-604-117
11	538	100.0	123	10	US-09-990-456-117
12	538	100.0	123	10	US-09-989-721-117
13	538	100.0	123	10	US-09-992-598-117
14	538	100.0	123	10	US-09-981-876-200
15	538	100.0	123	10	US-09-989-293A-117

PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/089514
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 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.08; Score 538; DB 9; Length 123;
 Best Local Similarity 100.08; Pred. No. 5e-51;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 LDALLVFGQVQLSCTSPQHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIP 60
 b 25 LDALLVFGQVQLSCTSPQHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIP 84
 Y 61 DRFSAKDEAHNACVLTISVPQEDDADYCVSYGYGSP 99
 b 85 DRFSAKDEAHNACVLTISVPQEDDADYCVSYGYGSP 123

RESULT 2

US-09-989-723-117
 Sequence 117, Application US/09989723
 Patent No. US20030072092A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC62

CURRENT APPLICATION NUMBER: US/09/989,723

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-15

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/091360
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PRIOR APPLICATION NUMBER: 60/091478

PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;

Best Local Similarity 100.0%; Pred. No. 5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDALLVFPQVQVQLSCTLSLSPQHVITRDYGVSWYQQRAGSAPRYLLYYRSEDDHRRPADIP 60
DB 25 LDALLVFPQVQVQLSCTLSLSPQHVITRDYGVSWYQQRAGSAPRYLLYYRSEDDHRRPADIP 84
QY 61 DRESAAKDEAHNACVLTISPQVEDDADYVCVGVGFSP 99
DB 85 DRESAAKDEAHNACVLTISPQVEDDADYVCVGVGFSP 123

RESULT 3

US-09-989-279-117

; Sequence 117, Application US/09989279

; Patent No. US20020072496A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-24

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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDALLVFGQVAQLSCTLSQHVITRDYGSWYQORAGSNPRVLLYYRSEEDHHRPADIP 60
DB 25 LDALLVFGQVAQLSCTLSQHVITRDYGSWYQORAGSNPRVLLYYRSEEDHHRPADIP 84

QY 61 DRFSAKDEAHNACVLTISVPQEDDADYVCVGYGFSP 99
DB 85 DRFSAKDEAHNACVLTISVPQEDDADYVCVGYGFSP 123

RESULT 4
US-09-989-727-117
Sequence 117, Application US/09989727
Patent No. US20020072497A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 LDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYYRSEDDHRRPADIP 84

QY 61 DRFSAKDEAHNACVLTITSPVQPEDDADYYCSGVGYGFSP 99
DB 85 DRFSAKDEAHNACVLTITSPVQPEDDADYYCSGVGYGFSP 123

RESULT 5
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; Sequence 117, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1998-04-28

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135 PRIOR APPLICATION NUMBER: 60/091360
136 PRIOR FILING DATE: 1998-07-01
137 PRIOR APPLICATION NUMBER: 60/091478
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145 PRIOR APPLICATION NUMBER: 60/091633
146 PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 LDALLVPPQVQLSCTISPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEDEHRRADIP 60
b 25 LDALLVPPQVQLSCTISPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEDEHRRADIP 84

y 61 DRESAAKDEAHNACVLTISPVQEDDADYYGVGVGFSP 99
b 85 DRESAAKDEAHNACVLTISPVQEDDADYYGVGVGFSP 123

RESULT 6

JS-09-989-732-117
Sequence 117, Application US/09989732

Patent No. US20020123463A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C57

CURRENT APPLICATION NUMBER: US/09/989,732

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. Se-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 LDALLVFPQGVQVQLSCTLSFQHVITRDYGVSWVQQRAGSAPRYLLYYRSEDDHHRPADIP 84

QY 61 DRFSAKDEAHNACVLTISFVQPEDDADYICVSGYGFSF 99
DB 85 DRFSAKDEAHNACVLTISFVQPEDDADYICVSGYGFSF 123

RESULT 7
US-09-991-073-117
; Sequence 117, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 538; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDALLVFPQVAQSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIP 60
DB 25 LDALLVFPQVAQSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIP 84

QY 61 DRFSAKDEARNACVLTISPVQPEDDADYCSVGYGFSF 99
DB 85 DRFSAKDEARNACVLTISPVQPEDDADYCSVGYGFSF 123

RESULT 8
US-09-990-442-117
Sequence 117, Application US/09990442
Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 5e-51;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 25 LDALLVFFGQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYYRSEDDHRRPADIP 84
QY 61 DFFSAKDEAHNACVLTITSPVQPEDDADYYCVSGYGFSP 99
Db 85 DFFSAKDEAHNACVLTITSPVQPEDDADYYCVSGYGFSP 123
RESULT 9
US-09-991-163-117
; Sequence 117, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Destroyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Caps 0;
1 LDALLVFGQVAQLSCILSPQHTVIRYGVSWYQQRAGSAPRYLLYVRSEDHRRADIP 60

QY

Db 25 LDALLVFPQVAQSLCTSPQHVITRDYGVSWYQQRAGSAPRYLLYYRSEEDHRRPADIP 84
QY 61 DRFSAKDEAHNACVLTSPVQPDADYICSVGYGFSP 99
Db 85 DRFSAKDEAHNACVLTSPVQPDADYICSVGYGFSP 123

RESULT 10
US-09-993-604-117
Sequence 117, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashtenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;

Best Local Similarity 100.0%; Pred. No. 5e-51; Indels 0; Gaps 0;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 85 DRFSAKDEAHNACVLITISVPQEDDADYYCSVGYGFSP 123

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US-09-990-456-117
Sequence 117, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;

Best Local Similarity 100.0%; Pred. No. 5e-51; Indels 0; Gaps 0;
Matches 99; Conservative 0; Mismatches 0;

QY	1	LDALLVFGVQAQISCTLSPOHVTIRDYGVSWTQOQAGSAPRYLLYYRSEEDHHRPADIP	60
DB	25	LDALLVFGVQAQISCTLSPOHVTIRDYGVSWTQOQAGSAPRYLLYYRSEEDHHRPADIP	84
QY	61	DRFSAAKDEAHNACVLITISFQPEDDADYCVSVGYGFSP	99
DB	85	DRFSAAKDEAHNACVLITISFQPEDDADYCVSVGYGFSP	123

RESULT 12
US-09-989-721-117
Sequence 117, Application US/09898721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deanoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Goddard, Audrey
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APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C55
CURRENT APPLICATION NUMBER: US/09/989,721
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/091633
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.08; Score 538; DB 10; Length 123;
Best Local Similarity 100.08; Pred. No. 5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDALLVFFQVQAQLSCTLSQPHVTIRDYGVSWYQORAGSAPRYLLYYRSEDDHRRPADIP 60
DB 25 LDALLVFFQVQAQLSCTLSQPHVTIRDYGVSWYQORAGSAPRYLLYYRSEDDHRRPADIP 84
QY 61 DRFSAKDEAHNACVLTISPVQPEDDADYICSVGVGSP 99
DB 85 DRFSAKDEAHNACVLTISPVQPEDDADYICSVGVGSP 123

RESULT 13

US-09-992-598-117
Sequence 117, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-09

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RESULT 14
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; Sequence 200, Application US/09981876
; Patent No. US2002016469A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P200191
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
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Query Match 100.0%; Score 538; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. NO. 5e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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25 LDALLVFGQVAQLSCTLSFQVHTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIP 84
61 DRFSAKDEAHNACVLTISPVQEDDADYVCVGYGFSP 99
85 DRFSAKDEAHNACVLTISPVQEDDADYVCVGYGFSP 123

RESULT 15
US-09-989-293A-117
Sequence 117, Application US/09989293A
Patent No. US2002017164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.

PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/08812
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
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PRIOR APPLICATION NUMBER: 60/090435

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 5e-51; Indels 0; Gaps 0;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDALLVFGQVAQLSCTLSPQHTVIRDYGVSWTQQRAGSAPRYLLYRSEEDHHRPADIP 60
Db 25 LDALLVFGQVAQLSCTLSPQHTVIRDYGVSWTQQRAGSAPRYLLYRSEEDHHRPADIP 84
QY 61 DRFSAKDEAHNAACVLTISPVEDDADYYCSVGYGFSP 99
Db 85 DRFSAKDEAHNAACVLTISPVEDDADYYCSVGYGFSP 123

Search completed: February 9, 2004, 12:56:23
Job time : 29.9865 secs

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M protein - protein search, using sw model

run on: February 9, 2004, 12:44:37 ; Search time 12.4865 Seconds
(without alignments)
335.465 Million cell updates/sec

title: US-09-981-876-200_COPY_25_123

effect score: 538

sequence: 1 LDALLVFEQVAQLSCTLSP.....PVQPEDDADYCVSGVGFSP 99

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 328717 seqs, 42310858 residues

total number of hits satisfying chosen parameters: 328717

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:**
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:**
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:**
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:**
- 5: /cgn2_6/ptodata/1/iaa/6C_COMB.pep:**
- 6: /cgn2_6/ptodata/1/iaa/6D_COMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	538	100.0	123	4	US-09-996-243-117
2	189	35.1	110	1	Sequence 117, App
3	189	35.1	110	2	Sequence 16, App
4	189.5	35.0	249	4	Sequence 16, App
5	184	34.2	109	3	Sequence 74, App
6	182.5	33.9	245	4	Sequence 42, App
7	181.5	33.7	110	3	Sequence 63, App
8	181	33.6	107	4	Sequence 34, App
9	181	33.6	107	4	Sequence 55, App
10	178.5	33.4	245	4	Sequence 48, App
11	178.5	33.2	245	4	Sequence 69, App
12	176.5	32.8	108	3	Sequence 14, App
13	176.5	32.8	111	2	Sequence 64, App
14	176.5	32.8	112	3	Sequence 65, App
15	175.5	32.6	110	3	Sequence 12, App
16	175.5	32.6	111	2	Sequence 20, App
17	175	32.5	108	4	Sequence 79, App
18	174.5	32.4	235	3	Sequence 155, App
19	174.5	32.4	244	4	Sequence 155, App
20	173.5	32.2	106	1	Sequence 15, App
21	173.5	32.2	106	1	Sequence 19, App
22	173.5	32.2	106	1	Sequence 19, App
23	173.5	32.2	106	1	Sequence 19, App
24	173.5	32.2	106	2	Sequence 155, App
25	173.5	32.2	106	2	Sequence 155, App
26	173.5	32.2	106	2	Sequence 155, App
27	173.5	32.2	106	3	Sequence 155, App

Sequence 155, App
Sequence 155, App
Sequence 51, App
Sequence 52, App
Sequence 32, App
Sequence 51, App
Sequence 39, App
Sequence 39, App
Sequence 33, App
Sequence 53, App
Sequence 19, App
Sequence 4, App
Sequence 47, App
Sequence 15, App
Sequence 35, App
Sequence 35, App
Sequence 49, App
Sequence 3, App

28 173.5 32.2 106 3 US-09-136-389-155
29 173.5 32.2 106 4 US-09-610-838-155
30 173.5 32.2 245 4 US-10-039-785-51
31 173.5 32.2 245 4 US-10-039-785-52
32 173 32.2 109 4 US-09-025-769B-32
33 173 32.2 109 4 US-09-025-769B-51
34 173 32.2 112 2 US-08-665-202-39
35 173 32.2 112 4 US-09-315-574-39
36 172.5 32.1 110 4 US-09-025-769B-33
37 172.5 32.1 110 4 US-09-025-769B-53
38 172.5 32.1 112 4 US-09-025-769B-19
39 172.5 32.1 131 1 US-08-305-683A-4
40 172.5 32.1 245 4 US-10-039-785-47
41 172 32.0 111 2 US-08-652-816A-15
42 171 31.8 97 2 US-08-665-202-35
43 171 31.8 97 4 US-09-315-574-35
44 171 31.8 104 3 US-09-240-274-49
45 171 31.8 278 3 US-09-260-527-3

ALIGNMENTS

RESULT 1
US-09-996-243-117
; Sequence 117, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCES: P2730F1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.4e-52;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 LDALLVPGGVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIP 60
25 LDALLVPGGVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIP 84
2Y 61 DRFSAAXDEAHNACVLITSPVQPEDDADYYCISVGYGFSP 99
25 DRFSAAXDEAHNACVLITSPVQPEDDADYYCISVGYGFSP 123

RESULT 2
US-07-988-925-16
Sequence 16, Application US/07988925
Patent No. 5585097
GENERAL INFORMATION:

APPLICANT: Bolt, Sarah L
APPLICANT: Clark, Michael R
APPLICANT: Gorman, Scott D
APPLICANT: Routledge, Edward G
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: antibody preparation
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon and Vanderhye pc
STREET: 11th Floor, 1100 No. 5585097th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988.925
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB92/01933
FILING DATE: 21-OCT-1992

ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-988-925-16

Query Match 35.1%; Score 189; DB 1; Length 110;
Best Local Similarity 46.4%; Pred. No. 9.1e-14;
Matches 39; Conservative 14; Mismatches 25; Indels 6; Gaps 2;

QY 8 PQOVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIPDRFSAAK 67
DB 14 PGKTVIISCTLSGN--IENNYVHWYQORPGAPTTFVIF-----DDDKRPGVDPDRFSGSI 67
QY 68 DEAHNACVLITSPVQPEDDADYYC 91
DB 68 DRSSNSASLTISGLQTEDEADYYC 91

RESULT 3
US-08-362-780-16
Sequence 16, Application US/08362780
Patent No. 5968509
GENERAL INFORMATION:

APPLICANT: Gorman, Scott D
APPLICANT: Routledge, Edward G
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: Antibody Preparation
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon and Vanderhye pc
STREET: 8th Floor, 1100 No. 5968509th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,780
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/862,543
FILING DATE: 23-JUNE-1992
APPLICATION NUMBER: GB 9021679.7
FILING DATE: 05-OCT-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB91/01726
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-362-780-16

Query Match 35.1%; Score 189; DB 2; Length 110;
Best Local Similarity 46.4%; Pred. No. 9.1e-14;
Matches 39; Conservative 14; Mismatches 25; Indels 6; Gaps 2;

QY 8 PQOVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIPDRFSAAK 67
DB 14 PGKTVIISCTLSGN--IENNYVHWYQORPGAPTTFVIF-----DDDKRPGVDPDRFSGSI 67
QY 68 DEAHNACVLITSPVQPEDDADYYC 91
DB 68 DRSSNSASLTISGLQTEDEADYYC 91

RESULT 4
US-08-918-148-74

; Sequence 74, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Guiney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 74
; LENGTH: 249
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-74

Query Match 35.0%; Score 188.5; DB 4; Length 249;
Best Local Similarity 49.4%; Pred. No. 2.7e-13;
Matches 42; Conservative 13; Mismatches 23; Indels 7; Gaps 3;
QY 8 PQGVAQLSCTSPQHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAK 67
DB 150 PQGVTISCTGSSGVGYNI-VSWYQCHPKAPKLIYGN-----NRSGVDFRFSK 204
QY 68 DEAHNACVLITSPQVEDDADYYCS 92
DB 205 --SGNTASLTISGLQAEDEADYFCS 227

RESULT 5
US-09-157-370-5
; Sequence 5, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEINBACHER, Stefan
; APPLICANT: STEINBACHER, Boris
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER FILING DATE: 1997-01-14
; EARLIER FILING DATE: 1997-01-14
; EARLIER FILING DATE: 1995-07-06
; EARLIER FILING DATE: 1995-07-06
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-157-370-5

Query Match 34.2%; Score 184; DB 3; Length 109;
Best Local Similarity 43.3%; Pred. No. 3.2e-13;
Matches 42; Conservative 15; Mismatches 24; Indels 16; Gaps 4;
QY 6 VFPQVAQLSCTSPQHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRFSA 65
DB 12 VSPGQTVITSCGDSLGIGY----VSWYQKPGQAPKLIY----DDNKRPSGIDPRFSG 63
QY 66 AKDEAHNACVLITSPQVEDDADYYC-----SVGYG 96
DB 64 SK--SGNTASLTISGLQAEDEADYFCSWSSSVVFG 98

RESULT 6
US-10-039-785-42
; Sequence 42, Application US/10039785

; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: P0550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 42
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A04 scFv
US-10-039-785-42

Query Match 33.9%; Score 182.5; DB 4; Length 245;
Best Local Similarity 45.9%; Pred. No. 1.2e-12;
Matches 39; Conservative 15; Mismatches 24; Indels 7; Gaps 3;
QY 8 PQGVAQLSCTSPQHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAK 67
DB 148 PQGVTISCTGTTSDVGNYI-VSWYQCHPKAPKLIYGVNQ----RPSGVDFRFSK 202
QY 68 DEAHNACVLITSPQVEDDADYYCS 92
DB 203 --SGNTASLTISGLQAEDEADYFCS 225

RESULT 7
US-09-240-274-63
; Sequence 63, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER FILING DATE: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER FILING DATE: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 63
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain O01
US-09-240-274-63

Query Match 33.6%; Score 181.5; DB 3; Length 110;
Best Local Similarity 44.0%; Pred. No. 6.8e-13;
Matches 37; Conservative 17; Mismatches 23; Indels 7; Gaps 3;

QY 8 PQGVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAK 67
DB 13 PGQRTVTSCTSSNIG-APGVHWYQPPGTAPKLVIY-----NDNRRPSGVDRFSGSK 67

QY 68 DEAHNACVLITSPVQPEDDADYVC 91
DB 68 --SGTSASLAITGLQAEADADYVC 89

RESULT 8
US-09-025-769B-34
; Sequence 34, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; APPLICATION DATE: 18-AUG-1995
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-34

Query Match 33.6%; Score 181; DB 4; Length 107;
Best Local Similarity 42.6%; Pred. No. 6.8e-13;
Matches 40; Conservative 13; Mismatches 31; Indels 10; Gaps 3;

QY 6 VFGQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSA 65
DB 12 VAPGQTARISCGD----ALGDKYASWYQKPGQAPVLVIY----DDSDRPSGIPERFSG 63

QY 66 AKDEAHNACVLITSPVQPEDDADYVC 99
DB 64 S--NSGNTATLITSGTQAEADADYVCQHHYTPP 95

RESULT 9
US-09-025-769B-55
; Sequence 55, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; APPLICATION DATE: 18-AUG-1995
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-55

Query Match 33.6%; Score 181; DB 4; Length 107;
Best Local Similarity 42.6%; Pred. No. 6.8e-13;
Matches 40; Conservative 13; Mismatches 31; Indels 10; Gaps 3;

QY 6 VFGQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSA 65
DB 12 VAPGQTARISCGD----ALGDKYASWYQKPGQAPVLVIY----DDSDRPSGIPERFSG 63

QY 66 AKDEAHNACVLITSPVQPEDDADYVC 99
DB 64 S--NSGNTATLITSGTQAEADADYVCQHHYTPP 95

RESULT 10
US-10-039-785-48
; Sequence 48, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PFE50
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05

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; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 245
; TYPE: PR1
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014F11 scFv
US-10-039-785-48

Query Match 33.4%; Score 179.5; DB 4; Length 245;
Best Local Similarity 45.9%; Pred. No. 2.7e-12; Gaps 3;
Matches 39; Conservative 13; Mismatches 26; Indels 7; Gaps 3;

QY 8 PQQVAQLSCTLSPQHVTIRDYGVSWTQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAAK 67
DB 148 PQQSVTISCTCTSDVGGYKY-VSWTQQHKGKAPKLMIV---EVSMPFSGVDRFSGSK 202
;
;
QY 68 DEAHNACVLITSPVQPEDDADYCS 92
;
;
DB 203 --SGNTASLTSGLQAEADYYCA 225
;
;
RESULT 11
US-10-039-785-49
; Sequence 49, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 245
; TYPE: PR1

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 12:55:12 / Search time 25 Seconds

(without alignments)
473.150 Million cell updates/sec

Title: US-09-981-876-200

Perfect score: 123

Sequence: 1 MACRLSFLMLGTFLSVSQ.....PVQPEDDADYCSGVGFSFP 123

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: PIR.76:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	8.9	123	2 S35302	B-cell protein 8HS
2	9	7.3	900	2 C71339	probable DNA misa
3	8	6.5	104	2 H90411	hypothetical prote
4	8	6.5	526	2 T21811	hypothetical prote
5	7	5.7	87	2 S16841	Ig kappa chain V r
6	7	5.7	93	2 T45245	hypothetical prote
7	7	5.7	109	2 S17381	hypothetical prote
8	7	5.7	123	2 S26264	T-cell receptor be
9	7	5.7	123	2 I38311	T-cell receptor be
10	7	5.7	145	2 C83370	cytochrome c oxida
11	7	5.7	191	2 C72411	Holliday junction
12	7	5.7	243	2 S27555	Ig lambda chain -
13	7	5.7	258	2 AB2317	hypothetical prote
14	7	5.7	265	2 B89837	hypothetical prote
15	7	5.7	272	2 F75412	spermidine/putresc
16	7	5.7	298	2 JQ2125	regulatory protein
17	7	5.7	322	1 S31087	phosphoprotein pho
18	7	5.7	340	1 C96665	permease (imported
19	7	5.7	371	2 G86851	histidyl-tRNA synt
20	7	5.7	375	2 AH2659	hypothetical prote
21	7	5.7	375	2 F97441	probable membrane
22	7	5.7	401	2 B64877	probable oxidoredu
23	7	5.7	401	2 D90861	probable oxidoredu
24	7	5.7	401	2 A85758	D-amino acid dehyd
25	7	5.7	418	2 A81228	Probable kynurenin
26	7	5.7	462	2 F75588	Probable membrane
27	7	5.7	464	2 AF0214	catalase (EC 1.11.
28	7	5.7	480	2 JC7672	hypothetical prote
29	7	5.7	484	2 B84254	hypothetical prote

30	7	5.7	518	2 E90944	probable transport
31	7	5.7	518	2 A85793	probable transport
32	7	5.7	518	2 H64942	hypothetical prote
33	7	5.7	519	2 AE0726	probable membrane
34	7	5.7	521	2 G84967	hypothetical prote
35	7	5.7	526	2 AD0770	probable membrane
36	7	5.7	528	2 AC0186	probable membrane
37	7	5.7	549	2 D90987	probable transport
38	7	5.7	549	2 G85832	probable transport
39	7	5.7	549	2 F64972	hypothetical prote
40	7	5.7	553	2 T27245	hypothetical prote
41	7	5.7	568	2 H88904	protein Y57GALC.9
42	7	5.7	659	2 T27246	hypothetical prote
43	7	5.7	837	1 S51680	fructose phosphor
44	7	5.7	934	2 I64819	DNA mismatch repai
45	7	5.7	937	2 B71612	hypothetical prote
46	6	4.9	51	2 S01870	hypothetical prote
47	6	4.9	54	2 S40381	Ig kappa chain V-I
48	6	4.9	54	2 A25521	Ig kappa chain V-I
49	6	4.9	60	2 A24626	Ig lambda chain V-
50	6	4.9	64	2 S17384	T-cell receptor be
51	6	4.9	72	2 T06599	disease resistance
52	6	4.9	77	2 D30502	Ig kappa chain V r
53	6	4.9	78	2 A47243	T-cell receptor be
54	6	4.9	78	2 C49039	T-cell receptor be
55	6	4.9	80	2 F75598	hypothetical prote
56	6	4.9	81	2 D83433	hypothetical prote
57	6	4.9	83	2 I30607	Ig kappa chain V-I
58	6	4.9	84	2 E28340	Ig kappa chain V r
59	6	4.9	87	2 S78490	Ig kappa chain V r
60	6	4.9	87	2 S16843	Ig kappa chain V r
61	6	4.9	87	2 S16823	Ig kappa chain V r
62	6	4.9	87	2 S16823	Ig kappa chain V r
63	6	4.9	89	2 S34096	Ig kappa chain V r
64	6	4.9	91	2 PH1071	Ig light chain V r
65	6	4.9	91	2 S37520	Ig kappa chain V r
66	6	4.9	91	2 S67940	Ig kappa chain V r
67	6	4.9	92	2 S37524	Ig kappa chain V r
68	6	4.9	92	2 S37513	Ig kappa chain V r
69	6	4.9	92	2 S37519	Ig kappa chain V r
70	6	4.9	92	2 S37517	Ig kappa chain V r
71	6	4.9	92	2 S37507	Ig kappa chain V r
72	6	4.9	92	2 S37502	Ig kappa chain V r
73	6	4.9	92	2 S37514	Ig kappa chain V r
74	6	4.9	92	2 S37510	Ig kappa chain V r
75	6	4.9	92	2 S37503	Ig kappa chain V r
76	6	4.9	92	2 S37518	Ig kappa chain V r
77	6	4.9	93	2 S37508	Ig kappa chain V r
78	6	4.9	93	2 S37526	Ig kappa chain V r
79	6	4.9	93	2 S37528	Ig kappa chain V r
80	6	4.9	93	2 S37501	Ig kappa chain V r
81	6	4.9	94	2 A70752	probable rpmB prot
82	6	4.9	95	2 F95332	hypothetical prote
83	6	4.9	96	2 S36060	Ig lambda chain -
84	6	4.9	96	2 PH1070	Ig light chain V r
85	6	4.9	96	2 B49442	Ig light chain V-I
86	6	4.9	96	2 A30601	Ig kappa chain V-I
87	6	4.9	98	2 S36068	Ig lambda chain -
88	6	4.9	98	2 S36050	Ig lambda chain -
89	6	4.9	99	1 W7WL35	E7 protein - human
90	6	4.9	99	2 S36055	Ig lambda chain -
91	6	4.9	99	2 S36056	Ig lambda chain -
92	6	4.9	99	2 S36057	Ig lambda chain -
93	6	4.9	99	2 S36058	Ig lambda chain -
94	6	4.9	99	2 JH0429	Ig kappa chain V-I
95	6	4.9	99	2 T37093	hypothetical prote
96	6	4.9	100	1 K3HUNG	Ig kappa chain pre
97	6	4.9	101	2 PH1057	Ig light chain V r
98	6	4.9	103	2 A38923	AL type amyloid fi
99	6	4.9	103	2 PH1056	Ig light chain V r
100	6	4.9	103	2 F70976	hypothetical prote

ALIGNMENTS

RESULT 1

S35302
B-cell protein SHS-20 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C:Accession: S35302
R/Shirasawa, T.; Ohnishi, K.; Hagiwara, S.; Shigenoto, K.; Takebe, Y.; Rajewsky, K.; Takemoto, J.; 1827-1834, 1993
A:Title: A novel gene product associated with mu chains in immature B cells.
A:Reference number: S35302; MUID:93259124; PMID:8491176
A:Accession: S35302
A:Molecule type: DNA
A:Residues: 1-123 <SH>
A:Cross-references: EMBL:D13208; NID:G286064; PIDN:BA02495.1; PID:G286065
C:Genetics:
A:Introns: 18/1
A:Gene: SHS-20
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: B-cell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-123/Product: B-cell protein SHS-20 #status predicted <MAT>

Query Match 8.9%; Score 11; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RPADIPDRFSA 89
|||||

Db 79 RPADIPDRFSA 89
|||||

RESULT 2

C71339
probable DNA mismatch repair protein (mutS) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: C71339
R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinther, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McQuibban, J.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: C71339
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-900 <COL>
A:Cross-references: GB:AE000520; NID:G3322597; PIDN:AAC65315.1; PID:G332260
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0328
C:Superfamily: DNA mismatch repair protein mutS

Query Match 7.3%; Score 9; DB 2; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 QQRAGSAPR 66
|||||

Db 807 QQRAGSAPR 815
|||||

RESULT 3

H90411
hypothetical protein SSO2405 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: H90411
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90411
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <KUR>
A:Cross-references: GB:AE006641; NID:G13815709; PIDN:AAK42551.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO2405

Query Match 6.5%; Score 8; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDALLY 30
|||||

Db 70 AQLDALLY 77
|||||

RESULT 4

T21811
hypothetical protein F35G12.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T21811
R/Chui, C.
submitted to the EMBL Data Library, October 1994
A:Reference number: Z19473
A:Accession: T21811
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-526 <WIL>
A:Cross-references: EMBL:Z46242; PIDN:CRA86334.1; GSPDB:GN00021; CESP:F35G12.12
A:Experimental source: clone F35G12
C:Genetics:
A:Gene: CESP:F35G12.12
A:Map position: 3
A:Introns: 12/3; 46/2; 82/3; 176/3; 240/3; 260/1; 381/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F35G12.12

Query Match 6.5%; Score 8; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQDAL 28
|||||

Db 208 VLAQDAL 215
|||||

RESULT 5

S16841
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16841
R/Blason, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid factor.
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16841
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-87 <BLA>
A:Cross-references: EMBL:X54839
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-82/Domain: immunoglobulin homology <IMM>

Query Match 5.7%; Score 7; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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A;Residues: 1-123 <PLA>
A;Cross-references: EMBL:X57613; NID:g37622; PIDN:CAA40839.1; PID:g37623
A;Experimental source: clone HT183
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;46-122/Domain: immunoglobulin homology <IMM>

Query Match          5.7%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89
    |||||
Db 89 IPDRFSA 95
    |||||

RESULT 9
I38311
T-cell receptor beta chain V region (V-beta 23, germline) precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
C;Accession: I38311
R;Slightom, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L.
Genomics 20, 149-168, 1994
A;Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor ge
A;Reference number: A54302; MUID:94292194; PMID:8020962
A;Accession: I38311
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <RES>
A;Cross-references: EMBL:U03115; NID:g467918; PIDN:AAA17710.1; PID:g467920
C;Genetics:
A;Gene: TCRBV23S1
A;Introns: 27/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;46-122/Domain: immunoglobulin homology <IMM>

Query Match          5.7%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89
    |||||
Db 89 IPDRFSA 95
    |||||

RESULT 10
C84370
cytochrome c oxidase subunit II [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84370
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leithausser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84370
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <STO>
A;Cross-references: GB:AE004437; NID:g10581612; PIDN:AAG20327.1; GSPDB:GN00138
C;Genetics:
A;Gene: coxB2

Query Match          5.7%; Score 7; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 PGQVAQL 38

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A;Residues: 1-109 <PER>
A;Cross-references: EMBL:X59799; NID:g33531; PIDN:CAA41605.1; PID:g312241
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;32-108/Domain: immunoglobulin homology <IMM>

Query Match          5.7%; Score 7; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89
    |||||
Db 75 IPDRFSA 81
    |||||

RESULT 8
S26264
T-cell receptor beta chain V region 5.5 precursor (clone HT183) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S26264
R;Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
J. Immunol. 147, 4360-4365, 1991
A;Title: New human V-beta genes and polymorphic variants.
A;Reference number: S26255; MUID:92091749; PMID:1684376
A;Accession: S26264
A;Molecule type: mRNA

Query Match          5.7%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GSAPRYL 68
    |||||
Db 23 GSAPRYL 29
    |||||

RESULT 7
I17381
T-cell receptor beta chain V region (clone IGB04) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: I17381
R;Ferradini, L.; Roman-Roman, S.; Azocar, J.; Michalaki, H.; Triebel, F.; Hercend, T.
Eur. J. Immunol. 21, 935-942, 1991
A;Title: Studies on the human T cell receptor alpha/beta variable region genes. II. Ident
A;Reference number: S17378; MUID:91209402; PMID:1826889
A;Accession: I17381
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <PER>
A;Cross-references: EMBL:X59799; NID:g33531; PIDN:CAA41605.1; PID:g312241
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;32-108/Domain: immunoglobulin homology <IMM>

Query Match          5.7%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GSAPRYL 68
    |||||
Db 23 GSAPRYL 29
    |||||

RESULT 6
45245
hypothetical protein MLCB1610.18 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T45245
R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z22949
A;Accession: T45245
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-93 <JAW>
A;Cross-references: EMBL:AL049913; PIDN:CA843164.1
A;Experimental source: cosmid B1610
C;Genetics:
A;Note: MLCB1610.18

```


Db 86 PQVLAQL 92
|||||
RESULT 11
C72411
Holliday junction DNA helicase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: C72411
R: Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72411
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-191 <ARN>
A:Cross-references: GB:AE001701; GB:AE000512; NID:G4980648; PIDN:AAD35258.1; PID:G498065
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0165
C:Superfamily: holliday junction DNA helicase ruva
Query Match 5.7%; Score 7; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 TFLVSQ 19
|||||
Db 52 TFLVSQ 58
RESULT 12
S25755
IG lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25755
R:Combrato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25755
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-243 <COM>
A:Cross-references: EMBL:X57820; NID:G33739; PIDN:CAA40957.1; PID:G33740
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:158-226/Domain: immunoglobulin homology <IMV>
Query Match 5.7%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 65 PRYLKY 71
|||||
Db 65 PRYLKY 71
RESULT 13
AB2317
Hypothetical protein all4089 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AB2317
R: Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuriitz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2317
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAF75788.1; PID:GI7133224; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4089
Query Match 5.7%; Score 7; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 QTVLAQL 25
|||||
Db 92 QTVLAQL 98
RESULT 14
B89837
Hypothetical protein SA0620 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: B89837
R: Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu, ma, A.; Mizutani-Ti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89837
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <KUR>
A:Cross-references: GB:BA000018; PID:GL3700556; PIDN:BAF41853.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0620
Query Match 5.7%; Score 7; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 LVFPQGV 35
|||||
Db 61 LVFPQGV 67
RESULT 15
F75412
spermidine/putrescine ABC transporter, permease protein - Deinococcus radiodurans (stra
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: F75412
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vanatavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567256
A:Accession: F75412
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <WHI>
A:Cross-references: GB:AE001977; GB:AE000513; NID:G6459045; PIDN:AAF10873.1; PID:G64590
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1303
A:Map position: 1
C:Superfamily: spermidine/putrescine transport system permease protein poth

```
Query Match      5.7%; Score 7; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 6 LSFLMG 12
    |||||
Db 244 LSFLMG 250

RESULT 16
regulatory protein trpI - Pseudomonas syringae
C:Species: Pseudomonas syringae
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JQ2125
R:Auerbach, S.; Gao, J.; Gussin, G.N.
Gene 123, 25-32, 1993
A:Title: Nucleotide sequences of the trpI, trpB, and trpA genes of Pseudomonas syringae
A:Reference number: JQ2125; MUID:93138427; PMID:8423001
A:Accession: JQ2125
A:Molecule type: DNA
A:Residues: 1-298 <AUE>
A:Cross-references: GB:M95710; NID:G151618; PIDN:AAA26015.1; PID:G151621
C:Genetics:
A:Gene: trpI
C:Superfamily: regulatory protein ampR
C:Keywords: DNA binding; transcription regulation

Query Match      5.7%; Score 7; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 25 LDALLVF 31
    |||||
Db 141 LDALLVF 147

RESULT 17
phosphoprotein phosphatase (EC 3.1.3.16) 1 (clone TOPP3) [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Nov-2001
C:Accession: S31087
R:Smith, R.D.; Walker, J.C.
Plant Mol. Biol. 21, 307-316, 1993
A:Title: Expression of multiple type 1 phosphoprotein phosphatases in Arabidopsis thaliana
A:Reference number: S31085; MUID:93144705; PMID:7678768
A:Accession: S31087
A:Molecule type: mRNA
A:Residues: 1-322 <SMI>
A:Cross-references: EMBL:M93410; NID:G166798; PIDN:AAA32838.1; PID:G166799
C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-spec
F:27-286/Domain: phosphoprotein phosphatase homology <PPP>
F:55-123/Domain: phosphoesterase core homology <PEC>
F:61,63,89/Binding site: iron (Asp, His, Asp) #status predicted
F:89,121,170,245/Binding site: zinc (Asp, Asn, His, His) #status predicted
F:92,122,269/Active site: Asp, His, Tyr #status predicted
F:93,218/Binding site: substrate phosphate (Arg) #status predicted

Query Match      5.7%; Score 7; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RPADIPD 85
    |||||
Db 188 RPADIPD 194

RESULT 18
phosphoprotein phosphatase (EC 3.1.3.16) 1 F22C12.20 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JQ2125
R:Auerbach, S.; Gao, J.; Gussin, G.N.
Gene 123, 25-32, 1993
A:Title: Nucleotide sequences of the trpI, trpB, and trpA genes of Pseudomonas syringae
A:Reference number: JQ2125; MUID:93138427; PMID:8423001
A:Accession: JQ2125
A:Molecule type: DNA
A:Residues: 1-298 <AUE>
A:Cross-references: GB:M95710; NID:G151618; PIDN:AAA26015.1; PID:G151621
C:Genetics:
A:Gene: trpI
C:Superfamily: regulatory protein ampR
C:Keywords: DNA binding; transcription regulation

Query Match      5.7%; Score 7; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 6 LSFLMG 12
    |||||
Db 244 LSFLMG 250

RESULT 16
regulatory protein trpI - Pseudomonas syringae
C:Species: Pseudomonas syringae
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JQ2125
R:Auerbach, S.; Gao, J.; Gussin, G.N.
Gene 123, 25-32, 1993
A:Title: Nucleotide sequences of the trpI, trpB, and trpA genes of Pseudomonas syringae
A:Reference number: JQ2125; MUID:93138427; PMID:8423001
A:Accession: JQ2125
A:Molecule type: DNA
A:Residues: 1-298 <AUE>
A:Cross-references: GB:M95710; NID:G151618; PIDN:AAA26015.1; PID:G151621
C:Genetics:
A:Gene: trpI
C:Superfamily: regulatory protein ampR
C:Keywords: DNA binding; transcription regulation

Query Match      5.7%; Score 7; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 25 LDALLVF 31
    |||||
Db 141 LDALLVF 147

RESULT 17
phosphoprotein phosphatase (EC 3.1.3.16) 1 (clone TOPP3) [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Nov-2001
C:Accession: S31087
R:Smith, R.D.; Walker, J.C.
Plant Mol. Biol. 21, 307-316, 1993
A:Title: Expression of multiple type 1 phosphoprotein phosphatases in Arabidopsis thaliana
A:Reference number: S31085; MUID:93144705; PMID:7678768
A:Accession: S31087
A:Molecule type: mRNA
A:Residues: 1-322 <SMI>
A:Cross-references: EMBL:M93410; NID:G166798; PIDN:AAA32838.1; PID:G166799
C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-spec
F:27-286/Domain: phosphoprotein phosphatase homology <PPP>
F:55-123/Domain: phosphoesterase core homology <PEC>
F:61,63,89/Binding site: iron (Asp, His, Asp) #status predicted
F:89,121,170,245/Binding site: zinc (Asp, Asn, His, His) #status predicted
F:92,122,269/Active site: Asp, His, Tyr #status predicted
F:93,218/Binding site: substrate phosphate (Arg) #status predicted

Query Match      5.7%; Score 7; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RPADIPD 85
    |||||
Db 188 RPADIPD 194

RESULT 18
phosphoprotein phosphatase (EC 3.1.3.16) 1 F22C12.20 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JQ2125
R:Auerbach, S.; Gao, J.; Gussin, G.N.
Gene 123, 25-32, 1993
A:Title: Nucleotide sequences of the trpI, trpB, and trpA genes of Pseudomonas syringae
A:Reference number: JQ2125; MUID:93138427; PMID:8423001
A:Accession: JQ2125
A:Molecule type: DNA
A:Residues: 1-298 <AUE>
A:Cross-references: GB:M95710; NID:G151618; PIDN:AAA26015.1; PID:G151621
C:Genetics:
A:Gene: trpI
C:Superfamily: regulatory protein ampR
C:Keywords: DNA binding; transcription regulation

Query Match      5.7%; Score 7; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LDALLVF 31
    |||||
Db 229 LDALLVF 235

RESULT 20
histidyl-tRNA synthetase hiss [imported] - Agrobacterium tumefaciens (strain C58, Dupont
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AH2659
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
```

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McLeish
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Accession: AB2577; MUID:21608550; PMID:11743193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-375 <KUR>
A:Cross-references: GB:AE008688; PIDN:AA141694.1; PID:g17739040; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: hisS
A:Map position: circular chromosome

Query Match 5.7%; Score 7; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDALL 29
|||||
Db 173 AQLDALL 179

RESULT 21
B64877
hypothetical protein AGR_C_1214 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: F97441
A:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: F97441
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-375 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86487.1; PID:g15155637; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_1214
A:Map position: circular chromosome

Query Match 5.7%; Score 7; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDALL 29
|||||
Db 173 AQLDALL 179

RESULT 22
B64877
probable membrane protein yciW - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: B64877
A:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B64877
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-401 <BLAT>
A:Cross-references: GB:AE000227; GB:U00096; NID:g1787543; PIDN:AACT4369.1; PID:g1787544;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:

A:Gene: yciW
C:Superfamily: Escherichia coli probable membrane protein yciW
C:Keywords: transmembrane protein
F:181-197/Domain: transmembrane #status predicted <TM>

Query Match 5.7%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 PDRESAA 90
|||||
Db 356 PDRESAA 362

RESULT 23

D90861
probable oxidoreductase ECs1860 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: D90861
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99829; MUID:21156231; PMID:11286796
A:Accession: D90861
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA835283.1; PID:g13361325; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs1860
C:Superfamily: Escherichia coli probable membrane protein yciW

Query Match 5.7%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 PDRESAA 90
|||||
Db 356 PDRESAA 362

RESULT 24

A85758
probable oxidoreductase yciW [imported] - Escherichia coli (strain O157:H7, substrain E
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A85758
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85758
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <STC>
A:Cross-references: GB:AE005174; NID:g12515501; PIDN:AA656525.1; GSPDB:GN00145; UWGP:Z2
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yciW
C:Superfamily: Escherichia coli probable membrane protein yciW

Query Match 5.7%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 PDRESAA 90
|||||
Db 356 PDRESAA 362

RESULT 25
1-amino acid dehydrogenase, small chain NME0176 [imported] - Neisseria meningitidis (strain
;Species: Neisseria meningitidis
;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
;Accession: A81228
;Tetlin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
;Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
;H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
;Science 287, 1809-1815, 2000
;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
;Reference number: A81000; MUID:20175755; PMID:10710307
;Accession: A81228
;Status: preliminary
;Molecule type: DNA
;Residues: 1-418 <TET>
;Cross-references: GB:AE002375; GB:AE002098; NID:g7225394; PIDN:AAF40633.1; PID:g722539
;Experimental source: serogroup B, strain MC58
;Genetics:
;Gene: NME0176

Query Match 5.7%; Score 7; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 20 TVLAQLD 26
| | | | |
b 259 TVLAQLD 265

RESULT 26
75588
probable kynureninase - Deinococcus radiodurans (strain R1)
;Species: Deinococcus radiodurans
;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
;Accession: F75588
;White, O.; Eisen, J.A.; Heideberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
;M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma
;S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
;Science 286, 1571-1577, 1999
;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
;Reference number: A75250; MUID:20036896; PMID:10567266
;Accession: F75588
;Status: preliminary
;Molecule type: DNA
;Residues: 1-462 <WHI>
;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12444.1; PID:g646073
;Experimental source: strain R1
;Genetics:
;Gene: DRA0338
;Map position: 2
;Superfamily: nifs protein

Query Match 5.7%; Score 7; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 22 LAQLDAL 28
| | | | |
b 62 LAQLDAL 68

RESULT 27
AF0214
probable membrane protein YP01759 [imported] - Yersinia pestis (strain CO92)
;Species: Yersinia pestis
;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
;Accession: AF0214
;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
;deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
;il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,

Nature 413, 523-527, 2001
;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
;Reference number: AB0001; MUID:21470413; PMID:11586360
;Accession: AF0214
;Status: preliminary
;Molecule type: DNA
;Residues: 1-464 <NUR>
;Cross-references: GB:AL590842; PIDN:CA90578.1; PID:gl5979786; GSPDB:GN00175
;Genetics:
;Gene: YP01759

Query Match 5.7%; Score 7; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLIM 11
| | | | |
Db 139 CLSFLIM 145

RESULT 28
JC7672
catalase (EC 1.1.1.6) - Desulfovibrio vulgaris
;Species: Desulfovibrio vulgaris
;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
;Accession: JC7672
;Kitamura, M.; Nakanishi, T.; Kojima, S.; Kumagai, I.; Inoue, H.
;J. Biochem. 129, 357-364, 2001
;Title: Cloning and expression of the catalase gene from the anaerobic bacterium Desul.
;Reference number: JC7672; MUID:21125589; PMID:11226874
;Accession: JC7672
;Molecule type: DNA
;Residues: 1-480 <KIT>
;Cross-references: DDBJ:AB020341
;Comment: This enzyme, one of the hemoproteins, located in the cytoplasm, functions as
;Genetics:
;Gene: kat
;Superfamily: catalase
;Keywords: oxidoreductase

Query Match 5.7%; Score 7; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 EDDADYY 114
| | | | |
Db 414 EDDADYY 420

RESULT 29
E84254
hypothetical protein Vng0983c [imported] - Halobacterium sp. NRC-1
;Species: Halobacterium sp. NRC-1
;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
;Accession: E84254
;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
;Lethausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
;Jung, K.H.; Alam, M.; Freitas, T.
;Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lu
;Title: Genome sequence of Halobacterium species NRC-1.
;Reference number: A84160; MUID:20504483; PMID:11016950
;Accession: E84254
;Status: preliminary
;Molecule type: DNA
;Residues: 1-484 <STO>
;Cross-references: GB:AE004437; NID:gl0580537; PIDN:AAI9401.1; GSPDB:GN00138
;Genetics:
;Gene: VNG0983C
;Superfamily: hypothetical protein MJ1633

Query Match 5.7%; Score 7; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 36;

Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	15	LSVQQT	21						
DB	287	LSVQQT	293						

RESULT 30
 E90944
 probable transport protein ECS2525 [imported] - Escherichia coli (strain O157:H7, subsp. C) Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C:Accession: E90944
 C:R:Hayashi, T.; Makino, K.; Kurckawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. G. Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; PMID:1156231; PMID:11258796
 A:Accession: E90944
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-518 <H>
 A:Cross-references: GB:BA000007; PIDN:BA835948.1; PID:gl3361992; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECS2525

Query Match	5.7%;	Score 7;	DB 2;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 38;		
Matches	7;	Conservative	0;	Mismatches 0;
				Indels 0;
Gaps	0;			

QY 5 CLSFLM 11
 |||||
 DB 189 CLSFLM 195

RESULT 31
 A85793
 probable transport protein yoaE [imported] - Escherichia coli (strain O157:H7, substrain C) Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A85793
 C:R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca, Nature 409, 528-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; PMID:21074935; PMID:11206551
 A:Accession: A85793
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-518 <S>
 A:Cross-references: GB:AB005174; NID:gl2515859; PIDN:AAG56805.1; GSPDB:GN00145; UWGP:Z28
 A:Experimental source: strain O157:H7, substrain EDU933
 C:Genetics:
 A:Gene: yoaE

Query Match	5.7%;	Score 7;	DB 2;	Length 518;
Best Local Similarity	100.0%;	Pred. No. 38;		
Matches	7;	Conservative	0;	Mismatches 0;
				Indels 0;
Gaps	0;			

QY 5 CLSFLM 11
 |||||
 DB 189 CLSFLM 195

RESULT 32
 H64942
 hypothetical protein b1816 - Escherichia coli (strain K-12) Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C:Accession: H64942
 C:R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.

```

Y      5 CLSFLM 11
b      189 CLSFLM 195

RESULT 35
D0770
robable membrane protein yegH [imported] - Salmonella enterica subsp. enterica serovar
;Species: Salmonella enterica subsp. enterica serovar Typhi
;Note: this species has also been called Salmonella typhi
;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
;Accession: AD0770
;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
h. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
ature 413, 848-852, 2001
;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
;Reference number: AB0502; MUID:21534947; PMID:11677608
;Accession: AD0770
;Status: preliminary
;Molecule type: DNA
;Residues: 1-526 <FAR>
;Cross-references: GB:AL513382; PIDN:CAD02482.1; PID:gl6503346; GSPDB:GN00176
;Genetics:
;Gene: yegH

Query Match      5.7%; Score 7; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11
b      189 CLSFLM 195

RESULT 36
AC0186
probable membrane protein YPO1527 [imported] - Yersinia pestis (strain CO92)
;Species: Yersinia pestis
;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
;Accession: AC0186
;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
;eno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
l, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
;Reference number: AB0001; MUID:21470413; PMID:11586360
;Accession: AC0186
;Status: preliminary
;Molecule type: DNA
;Residues: 1-528 <KUR>
;Cross-references: GB:AL590842; PIDN:CAC90350.1; PID:gl5979569; GSPDB:GN00175
;Genetics:
;Gene: YPO1527

Query Match      5.7%; Score 7; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11
b      189 CLSFLM 195

RESULT 37
D90987
probable transport protein ECs2868 [imported] - Escherichia coli (strain O157:H7, substra
;Species: Escherichia coli
;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
;Accession: D90987
;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen:
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90987
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-549 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA836291.1; PID:gl3362337; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 050952
C;Genetics:
A;Gene: ECs2868

Query Match      5.7%; Score 7; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11
b      211 CLSFLM 217

RESULT 38
G85832
probable transport protein yegH [imported] - Escherichia coli (strain O157:H7, substrain
;Species: Escherichia coli
;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
;Accession: G85832
;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85832
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-549 <STO>
A;Cross-references: GB:AE005174; NID:gl2516260; PIDN:AG57123.1; GSPDB:GN00145; UWGP:Z3.
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yegH

Query Match      5.7%; Score 7; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11
b      211 CLSFLM 217

RESULT 39
F64972
hypothetical protein b2063 - Escherichia coli (strain K-12)
;Species: Escherichia coli
;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
;Accession: F64972
;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64972
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-549 <BLAT>
A;Cross-references: GB:AE000296; GB:U00096; NID:gl788373; PIDN:AACT5124.1; PID:gl788377,
A;Experimental source: strain K-12, substrain MG1655

Query Match      5.7%; Score 7; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11

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```
Db      211 CLSFLM 217
|||||
RESULT 40
T27245
hypothetical protein Y57G11C.9a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27245
R:McMurray, A.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z20330
A:Accession: T27245
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-553 <WIL>
A:Cross-references: EMBL:Z99281; PIDN:CAB54458.1; GSPDB:GN00022; CESP:Y57G11C.9a
A:Experimental source: clone Y57G11C
C:Genetics:
A:Gene: CESP:Y57G11C.9a
A:Map position: 4
A:Introns: 67/2; 109/2; 382/1; 418/2; 447/1; 496/3
Query Match      5.7%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      24 QLDALLV 30
      |||||
Db      545 QLDALLV 551

RESULT 41
H88904
protein Y57G11C.9 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: H88904
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: AF5000; MUID:99069613; PMID:981916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88904
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-568 <STO>
A:Cross-references: GB:chr_IV; PIDN:CAB16531.1; PID:G3881206; GSPDB:GN00022; CESP:Y57G11
C:Genetics:
A:Gene: Y57G11C.9
A:Map position: 4
Query Match      5.7%; Score 7; DB 2; Length 568;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      24 QLDALLV 30
      |||||
Db      560 QLDALLV 566

RESULT 42
T27246
hypothetical protein Y57G11C.9b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27246
R:McMurray, A.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z20330
A:Accession: T27246
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-934 <RES>
A:Cross-references: GB:L47582; NID:G1000868; PIDN:AAB59565.1; PID:G1000869
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-659 <WIL>
A:Cross-references: EMBL:Z99281; PIDN:CAB54458.1; GSPDB:GN00022; CESP:Y57G11C.9b
A:Experimental source: clone Y57G11C
C:Genetics:
A:Gene: CESP:Y57G11C.9b
A:Map position: 4
A:Introns: 67/2; 109/2; 382/1; 418/2; 524/2; 553/1; 602/3
Query Match      5.7%; Score 7; DB 2; Length 659;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      24 QLDALLV 30
      |||||
Db      651 QLDALLV 657

RESULT 43
S51680
fructose phosphotransferase multiphosphoryltransfer protein - Xanthomonas campestris
N:Contains: phosphocarrier protein hpr; phosphotransferase system enzyme I (EC 2.7.3.9)
C:Species: Xanthomonas campestris
C:Date: 07-May-1995 #sequence_revision 31-Jan-1997 #text_change 11-Jun-1999
C:Accession: S51680
R:De Crecy-Lagard, V.; Danchin, A.
submitted to the EMBL Data Library, September 1994
A:Description: Phosphotransferase system of Xanthomonas campestris pv. campestris : cha
A:Reference number: S51680
A:Accession: S51680
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-837 <DEC>
A:Cross-references: EMBL:Z37113; NID:G603896; PIDN:CAA85482.1; PID:G603897
C:Genetics:
A:Gene: frub
A:Start codon: TTG
C:Superfamily: fructose phosphotransferase multiphosphoryltransfer protein; phosphotran
sferase system phosphohistidine-containing protein homology
C:Keywords: phosphocarrier protein; phosphohistidine; phosphoprotein; phosphotransferas
e; P22-145/Domain: phosphotransferase system mannitol-specific enzyme II factor III homol
F168-244/Domain: phosphotransferase system phosphohistidine-containing protein homology
F175-836/Domain: phosphotransferase system phosphohistidine-containing protein homology
F175/Active site: H18 (phosphohistidine intermediate) #status predicted
F206/Binding site: phosphate (Ser) (covalent) #status predicted
Query Match      5.7%; Score 7; DB 1; Length 837;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      21 VLAQLDA 27
      |||||
Db      406 VLAQLDA 412

RESULT 44
I64819
DNA mismatch repair protein - human
N:Alternate names: mismatch recognition protein MSH2; hereditary nonpolyposis cancer pro
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 17-Nov-2000
C:Accession: I64819; I51878; I64825; I64827; A49268; A49320; S41155; PC4190; I37550; S4
R:Wijnen, J.; Vasen, H.; Khan, P.M.; Menko, F.H.; van der Klift, H.; van Leeuwen, C.; v
Cats, A.; Kleibouker, J.; Varesco, L.; Bertario, L.; Bisgaard, M.L.; Mohr, J.; Fodde, R
Am. J. Hum. Genet. 56, 1060-1066, 1995
A:Title: Seven new mutations in hMSH2, an HNPCC gene, identified by denaturing gradient
A:Reference number: I51878; MUID:95243220; PMID:7726159
A:Accession: I64819
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-934 <RES>
A:Cross-references: GB:L47582; NID:G1000868; PIDN:AAB59565.1; PID:G1000869
```

QY 21 VLAQLDA 27

A;Cross-references: EMBL:X72491; NID:g441450; PIDN:CAA51159.1; PID:g441451
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 66; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 83 IPDRFS 88
DB 17 IPDRFS 22

RESULT 48

A25521
Ig kappa chain V region (321) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 09-May-1997
C;Accession: A25521
R;Chen, P.P.; Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, E.Y.; Schrantz, R.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986
A;Title: Genetic basis for the cross-reactive idiotypes on the light chains of human IGM
A;Reference number: A94135; MUID:87041448; PMID:3095834
A;Accession: A25521
A;Molecule type: DNA
A;Residues: 1-54 <CHE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 66; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 83 IPDRFS 88
DB 17 IPDRFS 22

RESULT 49

A24626
Ig lambda chain V-II region (Har) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
C;Accession: A24626
R;Sulitz, M.; Linke, R.
Biol. Chem. Hoppe-Seyler 366, 907-915, 1985
A;Title: Amyloid fibrils derived from V-region together with C-region fragments from a I
A;Reference number: A24626; MUID:86077295; PMID:3935132
A;Accession: A24626
A;Molecule type: Protein
A;Residues: 1-60 <EUL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 71; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 54 VSWYQQ 59
DB 28 VSWYQQ 33

RESULT 50

S17384
T-cell receptor beta chain V region (clone IGRb07) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S17384
R;Ferradini, L.; Roman-Roman, S.; Azocar, J.; Michalaki, H.; Triebel, F.; Hercend, T.
Eur. J. Immunol. 21, 935-942, 1991
A;Title: Studies on the human T cell receptor alpha/beta variable region genes. II. Ident
A;Reference number: S17378; MUID:91209402; PMID:1826889

A;Accession: S17384
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-64 <FER>
A;Cross-references: EMBL:X5804; NID:g33535; PIDN:CAA41610.1; PID:g33536
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 4.9%; Score 6; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 75; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 54 VSWYQQ 59
DB 2 VSWYQQ 7

RESULT 51

T06599
disease resistance response protein 230 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jun-2000
C;Accession: T06599
R;Chiang, C.C.; Hadwiger, L.A.
Mol. Plant Microbe Interact. 4, 324-331, 1991
A;Title: The Fusarium solani-induced expression of a pea gene family encoding high cyst
A;Reference number: Z15787; MUID:92190628; PMID:1799696
A;Accession: T06599
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-72 <CHI>
A;Cross-references: EMBL:L01578; NID:g169073; PIDN:AAA79117.1; PID:g169074
A;Experimental source: cv. Alaska
C;Genetics:
A;Gene: DRR230-a
C;Superfamily: gamma-thionin

Query Match 4.9%; Score 6; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 83; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 5 CLSFL 10
DB 8 CLSFL 13

RESULT 52

D30502
Ig kappa chain V region (D44) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999
C;Accession: D30502
R;Filat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m.
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: D30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-77 <EIL>
A;Cross-references: GB:M21908; NID:g197073; PIDN:AAA38908.1; PID:g197074
A;Note: the authors translated the codon CAG for residue 48 as Pro
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 88; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 54 VSWYQQ 59
DB 2 VSWYQQ 7

```

RESULT 53
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-80 <WHI>
A:Cross-references: GB:AE001862; GB:AE001825; NID:96460468; PIDN:AAF12357.1; PID:964606
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0052
A:Map position: 2

Query Match      4.9%; Score 6; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 AQLDAL 28
DB      53 AQLDAL 58

RESULT 54
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <STO>
A:Cross-references: GB:AE004597; GB:AE004091; NID:99947671; PIDN:AAG05100.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1711

Query Match      4.9%; Score 6; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 ISPVQP 107
DB       6 ISPVQP 11

RESULT 57
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <GON>
A:Cross-references: GB:AE001862; GB:AE001825; NID:96460468; PIDN:AAF12357.1; PID:964606
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0052
A:Map position: 2

Query Match      4.9%; Score 6; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 IPDRFS 88
DB      59 IPDRFS 64

```

```

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-80 <WHI>
A:Cross-references: GB:AE001862; GB:AE001825; NID:96460468; PIDN:AAF12357.1; PID:964606
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0052
A:Map position: 2

Query Match      4.9%; Score 6; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 AQLDAL 28
DB      53 AQLDAL 58

RESULT 56
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <STO>
A:Cross-references: GB:AE004597; GB:AE004091; NID:99947671; PIDN:AAG05100.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1711

Query Match      4.9%; Score 6; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 ISPVQP 107
DB       6 ISPVQP 11

RESULT 57
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <GON>
A:Cross-references: GB:AE001862; GB:AE001825; NID:96460468; PIDN:AAF12357.1; PID:964606
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0052
A:Map position: 2

Query Match      4.9%; Score 6; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 IPDRFS 88
DB      59 IPDRFS 64

```

```
RESULT 58
E28840
IG kappa chain V region (HP20) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 23-Jul-1999
C:Accession: E28840; L25114
R:Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBL J. 4, 3681-3698, 1985
A:Title: The idiotypic network and the internal image: possible regulation of a germ-line
A:Reference number: A91028; MUID:86136012; PMID:13937730
A:Accession: E28840
A:Molecule type: mRNA
A:Residues: 1-84 <OLL>
A:Cross-references: GB:X03385; NID:G52161; PIDN:CAA27112.1; PID:G52162
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 SWYQQR 60
Db 17 SWYQQR 22

RESULT 59
S78490
IG kappa chain V region (patient 31) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C:Accession: S78490; S34103
R:Wagner, S.
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
submitted to the EMBL Data Library, July 1992
A:Reference number: S78488
A:Accession: S78490
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: EMBL:X67187
A:Experimental source: patient 31
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34103
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-49, 'L', '51-61', 'YF', '64-75', 'A', '77-87' <WAW>
A:Cross-references: EMBL:X67187
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 50 IPDRFS 55

RESULT 60
S16843
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16843
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16843
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-87 <BLA>
A:Cross-references: EMBL:X54821
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 50 IPDRFS 55

RESULT 61
S16842
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16842
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16842
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-87 <BLA>
A:Cross-references: EMBL:X54840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 50 IPDRFS 55

RESULT 62
S16823
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16823
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16823
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-87 <BLA>
A:Cross-references: EMBL:X54821
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 50 IPDRFS 55
```

```

C;Keywords: heterotetramer; immunoglobulin

Query Match      4.9%; Score 6; DB 2; Length 91;
Best Local Similarity 100.0%; Pred.No.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 IPDRFS 88
      |||||
Db      42 IPDRFS 47

RESULT 66
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a human
A;Reference number: S67940; MUID:92314301; PMID:1617110
A;Accession: S67940
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <HEX>
A;Cross-references: EMBL:X73852
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match      4.9%; Score 6; DB 2; Length 91;
Best Local Similarity 100.0%; Pred.No.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 IPDRFS 88
      |||||
Db      40 IPDRFS 45

RESULT 67
S37524
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37524
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37524
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26620; NID:G405690; PIDN:CAA81373.1; PID:G405691
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match      4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred.No.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 IPDRFS 88
      |||||
Db      42 IPDRFS 47

RESULT 68
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37513
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
C;Superfamily: immunoglobulin V region; immunoglobulin homology

```

S37507
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37507
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A;Cross-references: EMBL:Z26605; NID:g405655; PIDN:CAA81358.1; PID:g405656
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
DB 42 IPDRFS 47

RESULT 72
S37502
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37502
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A;Cross-references: EMBL:Z26610; NID:g405645; PIDN:CAA81363.1; PID:g405646
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
DB 42 IPDRFS 47

RESULT 73
S37514
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37514
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A;Cross-references: EMBL:Z26597; NID:g405670; PIDN:CAA81351.1; PID:g405671
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
DB 42 IPDRFS 47

S37501
Reference number: S37501
Accession: S37513
Status: preliminary
Molecule type: mRNA
Residues: 1-92 <KLE>
Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81352.1; PID:g405669
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
DB 42 IPDRFS 47

RESULT 69
S37519
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37519
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A;Cross-references: EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; PID:g405681
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
DB 42 IPDRFS 47

RESULT 70
S37517
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37517
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A;Cross-references: EMBL:Z26615; NID:g405676; PIDN:CAA81368.1; PID:g405677
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
DB 42 IPDRFS 47

RESULT 71
S37517
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37517
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood
A;Cross-references: EMBL:Z26615; NID:g405676; PIDN:CAA81368.1; PID:g405677
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
DB 42 IPDRFS 47

```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y      83 IPDRFS 88
      |||||
b      42 IPDRFS 47

RESULT 74
37510
g kappa chain V region (V-kappa 3) - human (fragment)
;Species: Homo sapiens (man)
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
;Accession: S37510
;Klein, U.; Kuipers, R.; Rajewsky, K.
;Submitted to the EMBL Data Library, September 1993
;Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
;Reference number: S37501
;Accession: S37510
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-92 <KLE>
;Cross-references: EMBL:Z26601; NID:G405662; PIDN:CAA81355.1; PID:G405663
;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotrimer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y      83 IPDRFS 88
      |||||
b      42 IPDRFS 47

RESULT 75
37503
g kappa chain V region (V-kappa 3) - human (fragment)
;Species: Homo sapiens (man)
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
;Accession: S37503
;Klein, U.; Kuipers, R.; Rajewsky, K.
;Submitted to the EMBL Data Library, September 1993
;Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
;Reference number: S37501
;Accession: S37503
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-92 <KLE>
;Cross-references: EMBL:Z26609; NID:G405647; PIDN:CAA81362.1; PID:G405648
;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotrimer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y      83 IPDRFS 88
      |||||
b      42 IPDRFS 47

```

Search completed: February 9, 2004, 12:59:34
 Job time : 32 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

Run on: February 9, 2004, 12:49:12 ; Search time 18 Seconds
(without alignments)
321.349 Million cell updates/sec

Title: US-09-981-876-200

Perfect score: 123
Sequence: 1 MACRCLSLMGFLFSLVSQT.....PVQPEDDADYCSVGVGFSP 123

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	123	1	VPR3 HUMAN	O9uk13 homo sapien
2	9	7.3	900	1	MUTS TREPA	O83348 treponema p
3	7	5.7	188	1	RUVA THEME	O9wy12 thermotoga
4	7	5.7	298	1	TRPI PSESY	F34818 pseudomonas
5	7	5.7	320	1	YC19 KLEPN	O48445 klebsiella
6	7	5.7	322	1	PP13 ARATH	P48483 arabidopsis
7	7	5.7	401	1	YCIW ECOLI	P76035 escherichia
8	7	5.7	418	1	DADA NEIMB	O9klh5 neisseria m
9	7	5.7	515	1	V314 BUCAP	O8k9m0 buchnera ap
10	7	5.7	518	1	YOAE ECOLI	P76262 escherichia
11	7	5.7	521	1	Y323 BUCAI	P57408 buchnera ap
12	7	5.7	527	1	YEGH ECOLI	P76389 escherichia
13	7	5.7	934	1	MSH2 HUMAN	P43246 homo sapien
14	6	4.9	51	1	AC BFT4	P18924 bacterioph
15	6	4.9	72	1	D330 PEA	O01783 pisum sativ
16	6	4.9	94	1	R28A MYCTU	Q10879 mycobacteri
17	6	4.9	97	1	HLC2 TRVCR	P40368 trypanosoma
18	6	4.9	99	1	V57 HEPV35	P27230 human papil
19	6	4.9	100	1	KV3C HUMAN	P01621 homo sapien
20	6	4.9	108	1	KV3A HUMAN	P01619 homo sapien
21	6	4.9	108	1	LV3A HUMAN	P01714 homo sapien
22	6	4.9	109	1	KV3B HUMAN	P01620 homo sapien
23	6	4.9	109	1	KV3D HUMAN	P01622 homo sapien
24	6	4.9	109	1	KV3E HUMAN	P01623 homo sapien
25	6	4.9	109	1	KV3F HUMAN	P04206 homo sapien
26	6	4.9	109	1	KV3G HUMAN	P06888 homo sapien
27	6	4.9	109	1	LV2E HUMAN	P01708 homo sapien
28	6	4.9	110	1	LV2J HUMAN	P01713 homo sapien
29	6	4.9	111	1	LV1D HUMAN	P01702 homo sapien
30	6	4.9	111	1	LV2A HUMAN	P01704 homo sapien
31	6	4.9	111	1	LV2B HUMAN	P01705 homo sapien
32	6	4.9	111	1	LV2C HUMAN	P01706 homo sapien
33	6	4.9	111	1	LV2D HUMAN	P01707 homo sapien

RESULT 1

ALIGNMENTS

34	6	4.9	111	1	LV2F HUMAN	P01709 homo sapien
35	6	4.9	111	1	LV2G HUMAN	P01710 homo sapien
36	6	4.9	111	1	LV2H HUMAN	P01711 homo sapien
37	6	4.9	111	1	LV2I HUMAN	P01712 homo sapien
38	6	4.9	111	1	LV2L HUMAN	P04222 homo sapien
39	6	4.9	112	1	LV1H HUMAN	P06887 homo sapien
40	6	4.9	112	1	LV2K HUMAN	P04209 homo sapien
41	6	4.9	121	1	RNPA COXBU	P45648 coxiella bu
42	6	4.9	126	1	PCD5 MOUSE	P56812 mus musculu
43	6	4.9	128	1	KV3K HUMAN	P06311 homo sapien
44	6	4.9	129	1	KV3L HUMAN	P18135 homo sapien
45	6	4.9	129	1	KV3M HUMAN	P18136 homo sapien
46	6	4.9	130	1	LV1G HUMAN	P06316 homo sapien
47	6	4.9	136	1	KV5B MOUSE	P01634 mus musculu
48	6	4.9	142	1	VPR1 MOUSE	P13372 mus musculu
49	6	4.9	142	1	VPR2 MOUSE	P13373 mus musculu
50	6	4.9	169	1	RST1 AVESA	P50695 avena sativ
51	6	4.9	169	1	RST2 AVESA	P50696 avena sativ
52	6	4.9	169	1	RST3 AVESA	P50697 avena sativ
53	6	4.9	169	1	RST4 AVESA	P50698 avena sativ
54	6	4.9	172	1	PHCB SYN7	P50639 synechococc
55	6	4.9	173	1	HSIV YERPE	P08214 yersinia pe
56	6	4.9	174	1	VNSC PHODV	P35940 phocine dis
57	6	4.9	177	1	TLP OYSA	P31110 oryza sativ
58	6	4.9	189	1	CYOC BUCAP	O8k995 buchnera ap
59	6	4.9	190	1	APOM MOUSE	Q9zir3 mus musculu
60	6	4.9	190	1	APOM RAT	P14630 rattus norv
61	6	4.9	191	1	I18B MOUSE	Q920m9 mus musculu
62	6	4.9	199	1	VG66 B2MD2	O64258 mycobacteri
63	6	4.9	210	1	URK D3IRA	O9xz55 deinococcus
64	6	4.9	218	1	TRPF SYN3	P74435 synechocyst
65	6	4.9	234	1	GLNA DUNSA	P11600 dunaliella
66	6	4.9	234	1	YMFE ECOLI	P75968 escherichia
67	6	4.9	236	1	HIS4 RHOC	O30725 rhodobacter
68	6	4.9	236	1	SPSH STRPY	Q9X5C8 streptococc
69	6	4.9	237	1	NRL HUMAN	P54845 homo sapien
70	6	4.9	237	1	NRL MOUSE	P54846 mus musculu
71	6	4.9	237	1	UPK THEME	Q9WZ25 thermotoga
72	6	4.9	238	1	PSB6 MOUSE	Q60692 mus musculu
73	6	4.9	243	1	HIS4 BRUME	Q8ye36 bruceella me
74	6	4.9	243	1	HIS4 BRUSU	O81708 bruceella su
75	6	4.9	247	1	HIS4 AGRT5	P58790 agrobacteri
76	6	4.9	250	1	NGN2 HUMAN	Q9h2a3 homo sapien
77	6	4.9	251	1	C10B HUMAN	P02746 homo sapien
78	6	4.9	253	1	BTUD YERPE	Q8zdx6 yersinia pe
79	6	4.9	254	1	MODA HRAIN	P45323 haemophilus
80	6	4.9	256	1	TPIS VIBPA	Q87c31 vibrio para
81	6	4.9	259	1	Y128 CHLPN	Q92953 chlamydia p
82	6	4.9	262	1	END8 ECO57	Q8X9C6 escherichia
83	6	4.9	262	1	END8 ECOLI	P50465 escherichia
84	6	4.9	263	1	NGN2 MOUSE	P70447 mus musculu
85	6	4.9	255	1	COX3 MYTED	P41775 mytilus edu
86	6	4.9	277	1	HEMK ECOLI	P37186 escherichia
87	6	4.9	280	1	LPXC ANASP	Q8YU95 anabaena sp
88	6	4.9	280	1	MDCB KLEPN	P71422 klebsiella
89	6	4.9	283	1	PANC OCEIH	Q8CX59 oceanobacil
90	6	4.9	285	1	GSPC ERWCA	P31699 erwinia car
91	6	4.9	285	1	PPNK NEIMA	Q9Jq19 neisseria m
92	6	4.9	296	1	YGBJ ECOLI	Q46888 escherichia
93	6	4.9	302	1	TAL BUCAI	P57194 buchnera ap
94	6	4.9	316	1	TAL BUCAI	Q8ka27 buchnera ap
95	6	4.9	326	1	BLAA STRCI	P53651 scryptomyce
96	6	4.9	329	1	YE57 MYCPN	P75326 mycoplasma
97	6	4.9	333	1	NAUG METFL	Q50426 methylobact
98	6	4.9	336	1	NADA HELPJ	Q9zjnl helicobacte
99	6	4.9	341	1	Y33B MYCGE	Q9zb73 mycoplasma
100	6	4.9	344	1	ASTA ECOLI	P76218 escherichia

PR3 HUMAN STANDARD; PRT; 123 AA.
D VPR3_HUMAN
C Q9UK3; 2001 (Rel. 40, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 16-OCT-2001 (Rel. 42, Last annotation update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
E Pre-B lymphocyte protein 3 precursor (VpreB3 protein) (N27C7-2).
N VPREB3.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
M Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
N SEQUENCE FROM N.A.
P MEDLINE=20169186; PubMed=10702669;
A Rosnet O., Mattei M.-G., Delattre O., Schiff C.;
T "VPREB3: cDNA characterization and expression in human and chromosome
T mapping in human and mouse";
L Cytogenet. Cell Genet. 87:205-208 (1999).
N [2]
N SEQUENCE FROM N.A.
P Shimizu N., Minosima S., Kawasaki K., Sasaki T., Hosono K.;
A "Molecular cloning of N27C7-2 gene";
T Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
N [3]
N SEQUENCE FROM N.A.
P TISSUE=Testis;
X MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
A Brownstein M.J., Uedin T.B., Teshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullány S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fanev J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
A Butterfield V.S.N., Kryzhanovskiy M.I., Skalska U., Smalish D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length
T human and mouse cDNA sequences";
R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN B CELL PRECURSORS. EXPRESSED IN
CC FETAL LIVER, BONE MARROW, SPLEEN, AND LYMPH NODE.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; AF163825; AAF09451.1; -
CC EMBL; AB050772; BAB83034.1; -
CC EMBL; BC020666; AAH20666.1; -
CC HSSP; P01709; 2MCG.
CC Genew; HGNC:12710; VPREB3.
CC MIM; 605017;
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig MHC.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.

DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; B-cell; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 123 PRE-B LYMPHOCYTE PROTEIN 3.
FT DOMAIN 21 123 IG-LIKE.
FT DISULFID 40 115 BY SIMILARITY.
SQ SEQUENCE 123 AA; 13710 MW; BF09AC5196059E85 CRC64;
Query Match 100.0%; Score 123; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.3e-118; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0;
QY 1 MACRCLSFLMGTSLVSQTVLAQDLALFFPGVAQLSCTLSPOHVTIRDYGVSWYQQR 60
DB 1 MACRCLSFLMGTSLVSQTVLAQDLALFFPGVAQLSCTLSPOHVTIRDYGVSWYQQR 60
QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISVPQEDDADYYCSYGYG 120
DB 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISVPQEDDADYYCSYGYG 120
QY 121 FSP 123
DB 121 FSP 123
RESULT 2
MUTS_TREPA STANDARD; PRT; 900 AA.
ID MUTS_TREPA
AC O83348; 1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutS.
GN MUTS OR TP0328
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98327770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardnam J.W., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uetebach T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
R "Complete genome sequence of Treponema pallidum, the syphilis
R spirochete";
RL Science 281:375-388 (1998).
CC -!- FUNCTION: This protein is involved in the repair of mismatches in
CC DNA. It is possible that it carries out the mismatch recognition
CC step. This protein has a weak ATPase activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE001212; AAC65315.1; -
CC PIR; C71339; C71339.
CC TIGR; TP0328; -
CC HAMAP; MF 00096; 1.
CC InterPro; IPR005748; MutS1.
CC InterPro; IPR000432; MutS_C.
CC InterPro; IPR002863; MutS_N.
CC Pfam; PF01624; MutS_1; 1.


```

DR SMART: SM00278; HhH1; 2.
DR TIGRFAMs: TIGR00084; rva; 1.
DR DNA repair; SOS response; DNA-binding; DNA recombination; Helicase;
DR Complete proteome.
DR SEQUENCE 188 AA; 20818 MW; 2857F39D57FD61DD CRC64;

Query Match      5.7%; Score 7; DB 1; Length 188;
Best Local Similarity 100.0%; Pred.No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 13 TFLVSQ 19
   |||||
Db 49 TFLVSQ 55

RESULT 4
TRP1_PSEY STANDARD; PRT; 298 AA.
AC P34818;
CD 01-FEB-1994 (Rel. 28, Created)
DDT 01-FEB-1994 (Rel. 28, Last sequence update)
IDT 01-JUN-1994 (Rel. 29, Last annotation update)
DR TrpBA operon transcriptional activator.
GN TRP1
NC Pseudomonas syringae (pv. syringae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=321;
[1]
SEQUENCE FROM N.A.
MEDLINE=91318427; PubMed=8423001;
Auerbach S., gao J., Gussin G.N.;
"Nucleotide sequences of the trp1, trpB, and trpA genes of
Pseudomonas syringae: positive control unique to fluorescent
pseudomonads.";
Gene 123:25-32(1993).
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE
CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
-----
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CC or send an email to license@sb-sib.ch).
-----
CC EMBL; M95710; AAA26015.1; -.
CC FIR; JQ2125; JQ2125.
CC InterPro; IPR000847; HTH_LysR.
CC InterPro; IPR005119; LysR_subst.
CC Pfam; PF00126; HTH 1; 1.
CC Pfam; PF03466; LysR_substrate; 1.
CC PRINTS; PR00039; HTHLYSR.
CC PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
CC Tryptophan biosynthesis; Transcription regulation; Activator;
CC DNA-binding.
CC DNA BIND 23 42 H-T-H MOTIF (POTENTIAL).
CC SEQUENCE 298 AA; 32416 MW; 52D65FC34C15996B CRC64;

Query Match      5.7%; Score 7; DB 1; Length 298;
Best Local Similarity 100.0%; Pred.No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 25 LDALLVF 31
   |||||
Db 141 LDALLVF 147

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DR SMART: SM00278; HH1; 2.
DR TRIGRAMS: IIGR0084; ruva; 1.
RW DNA repair; SOS response; DNA-binding; DNA recombination; Helicase;
RW Complete protome.
SQ SEQUENCE 188 AA; 20818 MW; 2857F39D67FD61DD CRC64;

Query Match 5.7%; Score 7; DB 1; Length 188;
Best Local Similarity 100.0%; Pred.No.9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TFLVSQ 19
   |||||
Db 49 TFLVSQ 55

RESULT 4
TRP1_PSEY STANDARD; PRT; 298 AA.
ID TRP1_PSEY
AC P34819;
CD 01-FEB-1994 (Rel. 28, Created)
DD 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE TrpA operon transcriptional activator.
DN TRP1
GN Pseudomonas syringae (pv. syringae).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=321;
[1]
RRN SEQUENCE FROM N.A.
RRP MEDLINE=93138427; PubMed=8423001;
RFX Auerbach S., Gao J., Gusein G.N.;
RA "Nucleotide sequences of the trp1, trpB, and trpA genes of
RT Pseudomonas syringae: positive control unique to fluorescent
RRT pseudomonads.";
RRL Gene 123:25-32(1993).
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE
CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- REGULATORY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
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CC -----
CC EMBL; M95710; AAA26015.1; --
CC FIR; JQ2125; JQ2125.
CC InterPro; IPR000847; HTH_Lysr.
CC InterPro; IPR005119; Lysr_subst.
CC Pfam; PF00126; HTH_1; 1.
CC Pfam; PF03466; Lysr_substrate; 1.
CC PRINTS; PR00039; HTHLYSR.
CC PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
CC Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
KW DNA_BIND
FT SEQUENCE 298 AA; 32416 MW; 52D65FC34C15996B CRC64;
SQ

Query Match 5.7%; Score 7; DB 1; Length 298;
Best Local Similarity 100.0%; Pred.No.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LDALVF 31
   |||||
Db 141 LDALVF 147

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RESULT 5
YC19_KLEPN STANDARD; PRT; 320 AA.
AC Q48445;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in CFS region (ORF19) (Fragment).
DE Klebsiella pneumoniae
DE Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
DE Enterobacteriaceae; Klebsiella.
XX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Chedi;
RX MEDLINE=95204345; PubMed=7896702;
RA Arakawa Y., Wacharotayankun R., Nagatsuka T., Ito H., Kato N.,
RA "Genomic organization of the Klebsiella pneumoniae cps region
RT responsible for serotype K2 capsular polysaccharide synthesis in the
RT virulent strain Chedi."
RT J. Bacteriol. 177:1788-1796(1995).
RL J. Bacteriol. 177:1788-1796(1995).
CC -!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
CC -!- SIMILARITY: Contains 2 CBS domains.
CC -----
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CC -----
CC EMBL; D21242; BAA21009.1;
CC InterPro; IPR000644; CBS domain.
CC InterPro; IPR005170; CorC_HlyC.
CC InterPro; IPR005496; Terc.
CC Pfam; PF00571; CBS; 2.
CC Pfam; PF03471; CorC_HlyC; 1.
CC Pfam; PF03741; Terc; 1.
CC SMART; SM00116; CBS; 2.
KW Hypothetical protein; CBS domain; Repeat; Transmembrane.
FT TRANSMEM 24
FT NON_TER 320 320
FT SEQUENCE 320 AA; 36281 MW; 23F964B82E058D72 CRC64;
SQ
Query Match 5.7%; Score 7; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CLSFLM 11
DB 4 CLSFLM 10
RESULT 6
PP13_ARATH STANDARD; PRT; 322 AA.
AC P48483; Q9SH54;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein phosphatase PP1 isozyme 3 (EC 3.1.3.16).
GN TOPP3 OR ATIG64040 OR F22C12.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93144705; PubMed=7678768;
RA Smith R.D., Walker J.C.;

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RT "Expression of multiple type 1 phosphoprotein phosphatases in
RT Arabidopsis thaliana."
RL Plant Mol. Biol. 21:307-316(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Chung M.K., Conn L., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Egtu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Lagin-Hooper S., Lee A., Lee J.M., Ienz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vayaberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana".
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-1
CC SUBFAMILY.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M93410; AAA32838.1;
CC EMBL; AC007764; AAP24566.1; ALT_SEQ.
CC FIR; S31087; S31087.
CC HSPF; P08129; IFJM.
CC InterPro; IPR004843; M-peptidase.
CC InterPro; IPR006185; S/T phosphatase.
CC InterPro; IPR006186; T phosphatase.
CC Pfam; PF00149; Metallophos; 1.
CC PRINTS; PR00114; STPHPTASE.
CC ProDom; PD000252; T_phptase_apah; 1.
CC SMART; SM00156; PP2AC; 1.
CC HYDROLASE; PS00125; SER_THR_PHOSPHATASE; 1.
FT METAL 61 61
FT METAL 63 63
FT METAL 89 89
FT METAL 121 121
FT ACT_SITE 122 122
FT METAL 170 170
FT METAL 245 245
SQ SEQUENCE 322 AA; 36215 MW; 644A70BB9F63215C CRC64;
Query Match 5.7%; Score 7; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 RPADIPD 85
DB 188 RPADIPD 194
RESULT 7

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CW ECOLI
D YCIW ECOLI STANDARD; PRT; 401 AA.
T 15-JUL-1998 (Rel. 36, Created)
T 15-JUL-1998 (Rel. 36, Last sequence update)
T 15-OCT-2001 (Rel. 40, Last annotation update)
T Hypothetical protein yciW.
N YCIW OR B1287.
S Escherichia coli.
C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
C Enterobacteriaceae; Escherichia.
X NCBI_TaxID=562;
[1]
N SEQUENCE FROM N.A.
C STRAIN=K12 / MG1655;
X MEDLINE=97426617; PubMed=9278503;
A Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
A Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
A Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
A Mau B., Shao Y.;
T "The complete genome sequence of Escherichia coli K-12.";
L Science 277:1453-1474 (1997).
C -----
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C or send an email to license@isb-sib.ch).
C -----
R EMBL; AE000227; AAC74369.1; -.
R PIR; B64877; B64877.
R EcoGene; EG14262; yciW.
W Hypothetical protein; Complete proteome.
Q SEQUENCE 401 AA; 45130 MW; 1DF4FDCBEB9362B7 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 401;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 84 PDRFSAA 90
b 356 PDRFSAA 362
|||||

RESULT 8
D DADA NEIMB STANDARD; PRT; 418 AA.
C Q9K1H5.
Y 28-FEB-2003 (Rel. 41, Created)
Y 28-FEB-2003 (Rel. 41, Last sequence update)
Y 28-FEB-2003 (Rel. 41, Last annotation update)
DE D-amino acid dehydrogenase small subunit (EC 1.4.99.1).
N DADA OR NMB0176.
S Neisseria meningitidis (serogroup B).
C Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
C Neisseriaceae; Neisseria.
X NCBI_TaxID=491;
[1]
N SEQUENCE FROM N.A.
R STRAIN=MC58 / Serogroup B;
C MEDLINE=20175755; PubMed=10710307;
Y Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Y Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Y Nelson W.C., Gwin M.L., DeSoy R., Peterson J.D., Hickey E.K.,
Y Hat D.H., Salzberg S.B., White O., Fleischmann R.D., Dougherty B.A.,
Y Mason T., Ciecko A., Parkey D.S., Blair E., Ciftone H., Clark E.B.,
Y Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Y Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
Y Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
X "Complete genome sequence of Neisseria meningitidis serogroup B strain
X MC58.";
```

```

RL Science 287:1809-1815 (2000).
CC -!- FUNCTION: Oxidative deamination of D-amino acids (By similarity).
CC -!- CATALYTIC ACTIVITY: A D-amino acid + H(2)O + acceptor = a 2-oxo
CC acid + NH(3) + reduced acceptor.
CC -!- COFACTOR: FAD (By similarity).
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE DADA FAMILY OF OXIDOREDUCTASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
R EMBL; AE002375; AAF40633.1; -.
R PIR; A81228; A81228.
R TIGR; NMB0176; -.
R HAMAP; MF_01202; -.
R InterPro; IPR006076; IPR006076.
R InterPro; IPR00205; NAD_binding.
R Pfam; PF01266; DAO; 1.
KW Oxidoreductase; Flavoprotein; FAD; Complete proteome.
FT NP_BIND 3 17
SQ SEQUENCE 418 AA; 46335 MW; B50C13F9DFBC214D CRC64;

Query Match 5.7%; Score 7; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 TVLAQLD 26
DB 259 TVLAQLD 265
|||||

RESULT 9
Y314 BUCAP STANDARD; PRT; 515 AA.
ID Y314 BUCAP
AC Q8K9NC;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein BUSG314.
GN BUSG314.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
[1]
N SEQUENCE FROM N.A.
R MEDLINE=22084549; PubMed=12089438;
R Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
R Werngreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
R "50 million years of genomic stasis in endosymbiotic bacteria.";
R Science 296:2376-2379 (2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY. STRONG, TO E.COLI YOAE.
CC -!- SIMILARITY: Contains 2 CBS domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
R EMBL; AE014108; AAM67868.1; -.
R InterPro; IPR000644; CBS domain.
R InterPro; IPR005170; CorC_HlyC.
R InterPro; IPR005496; Terc.
```

DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF03471; CoxC HlyC; 1.
 DR Pfam; PF03741; TerC; 1.
 KW Hypothetical protein; CBS domain; Repeat; Transmembrane;
 WT Complete proteome.
 TT TRANSMEM 14 34 POTENTIAL.
 TT TRANSMEM 49 69 POTENTIAL.
 TT TRANSMEM 79 99 POTENTIAL.
 TT TRANSMEM 125 145 POTENTIAL.
 TT TRANSMEM 150 170 POTENTIAL.
 TT TRANSMEM 185 205 POTENTIAL.
 TT TRANSMEM 207 227 POTENTIAL.
 T TRANSMEM 207 227 POTENTIAL.
 Q SEQUENCE 515 AA; 57607 MW; 4BP8D4A88BCA1901 CRC64;
 Query Match 5.7%; Score 7; DB 1; Length 515;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 5 CLSFLM 11
 |||||
 Db 189 CLSFLM 195

RESULT 10
 COAE ECOLI STANDARD; PRT; 518 AA.
 LC P76262; 1997 (Rel. 35, Created)
 JT 01-NOV-1997 (Rel. 35, Last sequence update)
 JT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein yoaE.
 NV YOA E OR B1816 OR C2222 OR Z2859 OR ECS2525.
 VS Escherichia coli.
 VS Escherichia coli O6, and
 VS Escherichia coli O157:H7.
 JC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 JC Enterobacteriaceae; Escherichia.
 NCBI_Taxid=562, 217992, 83334;
 [1]
 RP SEQUENCE FROM N.A.
 IC STRAIN=K12 / MG1655;
 XX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 [2]
 RP SEQUENCE FROM N.A.
 IC STRAIN=K12;
 XX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H.,
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
 RA "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 40.1-50.0 min region on the linkage map."
 RL DNA Res. 3:379-392(1996).
 [3]
 RP SEQUENCE FROM N.A.
 IC STRAIN=O6:H1 / CFT073 / ATCC 700928;
 XX MEDLINE=22386234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 [4]

RP SEQUENCE FROM N.A.
 IC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 XX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
 RL Nature 409:529-533(2001).
 [5]
 RP SEQUENCE FROM N.A.
 IC STRAIN=O157:H7 / RIMD 0509952;
 XX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Kan C.-G., Ohsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12."
 RL DNA Res. 8:11-22(2001).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
 CC -!- SIMILARITY: Contains 2 CBS domains.
 CC
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 CC
 CC EMBL; AE000276; AAC74886.1; -
 DR EMBL; D30835; BAA15623.1; -
 DR EMBL; D30836; BAA15628.1; -
 DR EMBL; AE016761; AAN80681.1; -
 DR EMBL; AE005404; AAG56805.1; -
 DR EMBL; AF002558; BAB35948.1; -
 DR PIR; E90944; E90944.
 DR PIR; H64942; H64942.
 DR EcoGene; EGI3517; yoaE.
 DR InterPro; IPR000644; CBS domain.
 DR InterPro; IPR005170; CoxC HlyC.
 DR InterPro; IPR005496; TerC.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF03471; CoxC HlyC; 1.
 DR Pfam; PF03741; TerC; 1.
 KW Hypothetical protein; CBS domain; Repeat; Transmembrane;
 KW Complete proteome.
 FT TRANSMEM 14 34 POTENTIAL.
 FT TRANSMEM 49 69 POTENTIAL.
 FT TRANSMEM 79 99 POTENTIAL.
 FT TRANSMEM 125 145 POTENTIAL.
 FT TRANSMEM 150 170 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT TRANSMEM 355 375 POTENTIAL.
 SQ SEQUENCE 518 AA; 56527 MW; 90DF7C9A092F1ECC CRC64;
 Query Match 5.7%; Score 7; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 CLSFLM 11
 |||||
 Db 189 CLSFLM 195

RESULT 11
 Y323_BUCAI STANDARD; PRT; 521 AA.
 ID Y323_BUCAI

P57408;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein BU323.
Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
NCBI_TaxID=118099;
[1]
SEQUENCE FROM N.A.
STRAIN=Tokyo 1998;
MEDLINE=20445173; PubMed=1093077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
Nature 418:81-86(2000).
A 460-Kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE UPF0053 FAMILY. STRONG, TO E.COLI Y0AE.
-1- SIMILARITY: Contains 2 CBS domains.
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EMBL; AP001119; BAB13031.1; -
InterPro; IPR000644; CBS domain.
InterPro; IPR005170; CorC HlyC.
InterPro; IPR005496; TerC.
Pfam; PF00571; CBS; 2.
Pfam; PF03471; CorC HlyC; 1.
Hypothetical protein; CBS domain; Repeat; Transmembrane; Complete proteome.
TRANSMEM 13 33 POTENTIAL.
TRANSMEM 49 69 POTENTIAL.
TRANSMEM 80 100 POTENTIAL.
TRANSMEM 125 145 POTENTIAL.
TRANSMEM 150 170 POTENTIAL.
TRANSMEM 185 205 POTENTIAL.
TRANSMEM 207 227 POTENTIAL.
SEQUENCE 521 AA; 58722 MW; 56D9E406600DD958 CRC64;
Query Match 5.7%; Score 7; DB 1; Length 521;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 5 CLSFLM 11
| | | | |
D 189 CLSFLM 195
RESULT 12
EGH_ECOLI STANDARD; PRT; 527 AA.
AC P76389; P94756;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yegH.
YEGH OR B2063.
Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
[1]
SEQUENCE FROM N.A.

RC STRAIN=KL2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
[2]
SEQUENCE FROM N.A.
RC STRAIN=KL2;
MEDLINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitagawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., Sampaio G., Seki Y., Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
"A 460-Kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
-1- SIMILARITY: Contains 2 CBS domains.
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EMBL; AB000296; AAC75124.1; ALT INIT.
EMBL; D90844; BAA15916.1; ALT_INIT.
ECOGene; EGI4051; YegH.
InterPro; IPR000644; CBS domain.
InterPro; IPR005170; CorC HlyC.
InterPro; IPR005496; TerC.
Pfam; PF00571; CBS; 2.
Pfam; PF03471; CorC HlyC; 1.
Pfam; PF03741; TerC; 1.
SMART; SM00116; CBS; 2.
Hypothetical protein; CBS domain; Repeat; Transmembrane; Complete proteome.
TRANSMEM 14 34 POTENTIAL.
TRANSMEM 81 71 POTENTIAL.
TRANSMEM 81 101 POTENTIAL.
TRANSMEM 145 165 POTENTIAL.
TRANSMEM 185 205 POTENTIAL.
SEQUENCE 527 AA; 59450 MW; 0C211895B9A0112D CRC64;
Query Match 5.7%; Score 7; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 5 CLSFLM 11
| | | | |
D 189 CLSFLM 195
RESULT 13
MSH2_HUMAN STANDARD; PRT; 934 AA.
AC P43246; O75488;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
DNA mismatch repair protein Msh2.
MSH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=94073959; PubMed=8252616;
Fishel R., Lescoe M., Rao M., Copeland N.G., Jenkins N.A.,
Garber J., Kane M.F., Kolodner R.D.;
"The human mutator gene homolog MSH2 and its association with
hereditary nonpolyposis colon cancer.";
Cell 75:1027-1038(1993).
[2]
[3]
ERRATUM.
MEDLINE=94208055; PubMed=8156592;
Fishel R., Lescoe M., Rao M., Copeland N.G., Jenkins N.A.,
Garber J., Kane M.F., Kolodner R.D.;
Cell 77:167-167(1994).
[4]
[5]
SEQUENCE FROM N.A. AND DISSE.
MEDLINE=95229152; PubMed=7713503;
Kolodner R.D., Hall N.R., Lipford J., Kane M.F., Rao M.R.S.,
Morrison P., Wirth L., Finan P., Burn J., Chapman P., Earabino C.,
Merchant E., Bishop D.T.;
"Structure of the human MSH2 locus and analysis of two Muir-Torre
kindreds for msh2 mutations.";
Genomics 24:516-526(1994).
[6]
[7]
SEQUENCE FROM N.A.
TISSUE=Muscle;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Faney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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human and mouse cDNA sequences.";
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SEQUENCE OF 375-425 FROM N.A.
TISSUE=Blood;
Corvello C.M., Bevilacqua R.A.U., Rossi B.M., Simpson A.J.G.;
"A novel germline mutation at exon 7 of the hMSH2 gene (417 del G) in
a large HNPCC Brazilian kindred.";
Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
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DNA-BINDING.
MEDLINE=95007585; PubMed=7923193;
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"Purified human MSH2 protein binds to DNA containing mismatched
nucleotides.";
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MEDLINE=20245492; PubMed=10783165;
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"BASC, a super complex of BRCA1-associated proteins involved in the
recognition and repair of aberrant DNA structures.";
Genes Dev. 14:927-939(2000).
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REVIEW.
MEDLINE=94310688; PubMed=8036718;
Jiricny J.,

RT "Colon cancer and DNA repair: have mismatches met their match?";
Trends Genet. 10:164-168(1994).
RN [9]
RP REVIEW ON VARIANTS.
RX MEDLINE=97403931; PubMed=9259192;
RA Papadopoulos N., Lindblom A.;
RT "Molecular basis of HNPCC: mutations of MMR genes.";
Hum. Mutat. 10:89-99(1997).
RN [10]
RP VARIANTS HNPCC LEU-622 AND TYR-639.
RX MEDLINE=94084796; PubMed=8261515;
RA Leach F.S., Nicolaides N.C., Papadopoulos N., Liu B., Jen J.,
Parsons R., Peltomaki P., Sistonen P., Aaltonen L.A.,
Nystrom-Lahti M., Guan X.-Y., Zhang J., Meltzer P.S., Yu J.-W.,
Kao F.-T., Chen D.J., Cerosaletti K.M., Pournier R.E.K., Todd S.,
Lewis T., Leach R.J., Naylor S.L., Weissenbach J., Mecklin J.-P.,
Jaarvinen H., Petersen G.M., Hamilton S.R., Green J., Jass J.,
Watson P., Lynch H.T., Trent J.M., de la Chapelle A., Kinzler K.W.,
Vogelstein B.;
RT "Mutations of a muts homolog in hereditary nonpolyposis colorectal
cancer.";
Cell 75:1215-1225(1993).
RN [11]
RP VARIANT HNPCC ASN-596 DEL.
RX MEDLINE=95179130; PubMed=7874129;
RA Mary J.-L., Bishop T., Kolodner R.D., Lipford J.R., Kane M.F.,
Weber W., Torhorst J., Mueller H., Spycher M., Scott R.J.;
RT "Mutational analysis of the hMSH2 gene reveals a three base pair
deletion in a family predisposed to colorectal cancer development.";
Hum. Mol. Genet. 3:2067-2069(1994).
RN [12]
RP VARIANT HIS-96.
RX MEDLINE=95243220; PubMed=7726159;
RA Wijnen J., Vassen H., Khan P.M., Menko F.H., van der Klift H.,
van Leeuwen C., van den Broek M., van Leeuwen-Cornelisse I.,
Ngeingast F., Weijers-Heijboer A., Lindhout D., Griffioen G., Cats A.,
Kleibeker J., Varesco L., Bertario L., Bisgaard M.-L., Mohr J.,
Fodde R.;
RT "Seven new mutations in hMSH2, an HNPCC gene, identified by
denaturing gradient-gel electrophoresis.";
Am. J. Hum. Genet. 56:1060-1066(1995).
RN [13]
RP VARIANTS PHR-390 AND LYS-419.
RX MEDLINE=96305099; PubMed=8690195;
RA Konishi M., Kikuchi-Yanoshita R., Tanaka K., Muraoka M., Onda A.,
Okumura Y., Kishi N., Iwama T., Mori T., Koike M., Ushio K., Chiba M.,
Nomizu S., Konishi F., Utsunomiya J., Miyaki M.;
RT "Molecular nature of colon tumors in hereditary nonpolyposis colon
cancer, familial polyposis, and sporadic colon cancer.";
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RN [14]
RP VARIANT ASP-322.
RX MEDLINE=96163505; PubMed=8566964;
RA Maliaka Y.K., Chudina A.P., Belev N.F., Alday P., Bochkov N.P.,
Buerstedde J.-M.;
RT "CpG dinucleotides in the hMSH2 and hMLH1 genes are hotspots for
HNPCC mutations.";
Hum. Genet. 97:251-255(1996).
RN [15]
RP VARIANT HNPCC ASN-596 DEL, AND VARIANT HIS-167.
RX MEDLINE=97026284; PubMed=8872463;
RA Moslein G., Tester D.J., Lindor N.M., Honechel R., Cunningham J.M.,
French A.J., Halling K.C., Schwab M., Gorzki P., Thibodeau S.N.;
RT "Microsatellite instability and mutation analysis of hMSH2 and hMLH1
in patients with sporadic, familial and hereditary colorectal
cancer.";
Hum. Mol. Genet. 5:1245-1252(1996).
RN [16]
RP VARIANT CRC TYR-506.
RX MEDLINE=96390800; PubMed=8797773;
RA Han H.-J., Yuan Y., Xu J.-L., Oh J.-H., Won Y.-J., Kang K.J.,
Kim K.-Y., Kim S., Kim C.Y., Kim J.-P., Oh N.-G., Lee K.H., Choe K.J.,
Nakamura Y., Park J.-G.;

T "Germline mutations of hMLH1 and hMSH2 genes in Korean hereditary
T nonpolyposis colorectal cancer.";
J Natl. Cancer Inst. 88:1317-1319(1996).
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N VARIANT GLN-46.
P MEDLINE=96293410; PubMed=8700523;
X Bubb V.J., Curtis L.J., Cunningham C., Dunlop M.G., Carothers A.D.,
A Morris R.G., White S., Bird C.C., Wyllie A.H.,
T "Microsatellite instability and the role of hMSH2 in sporadic
T colorectal cancer";
L Oncogene 12:2641-2649(1996).
N [18]
P VARIANTS HNPCC THR-305; THR-834 AND ASN-596 DEL.
X MEDLINE=97456423; PubMed=93111737;
X Wijnen J., Khan P.M., Vasen H., van der Klift H., Mulder A.,
A van Leeuwen-Cornelisse I., Bakker B., Loekeoot M., Moeller P.,
A Podde R.;
T "Hereditary nonpolyposis colorectal cancer families not complying
T with the Amsterdam criteria show extremely low frequency of
T mismatch-repair-gene mutations.";
L Am. J. Hum. Genet. 61:329-335(1997).
N [19]
P VARIANT HNPCC CYS-323.
X MEDLINE=97382414; PubMed=9240418;
A Akiyama Y., Teubouchi N., Yuasa Y.;
T "Frequent somatic mutations of hMSH3 with reference to microsatellite
T instability in hereditary nonpolyposis colorectal cancers.";
L Biochem. Biophys. Res. Commun. 236:248-252(1997).
N [20]
P VARIANT SER-596.
X MEDLINE=97147120; PubMed=8993976;
A Viel A., Genuardi M., Capozzi E., Leonardi F., Bellacosa A.,
A Paravatou-Petsotas M., Pomponi M.G., Fornasari M., Percesepe A.,
A Roncucci L., Ramassia M.G., Benatti P., Ponz de Leon M., Valenti A.,
A Covino M., Anti M., Foletto M., Bolocchi M., Neri G.;
T "Characterization of MSH2 and MLH1 mutations in Italian families with
T hereditary nonpolyposis colorectal cancer.";
L Genes Chromosomes Cancer 18:8-18(1997).
N [21]
P VARIANT ASP-322.
X MEDLINE=97242567; PubMed=9087566;
A Wu Y., Nyström-Lahti M., Osinga J., Looman M.W.G., Peltomäki P.,
A Aaltonen L.A., de la Chapelle A., Hofstra R.M.W., Buys C.H.C.M.;
T "MSH2 and MLH1 mutations in sporadic replication error-positive
Query Match 5.7%; Score 7; DB 1; Length 934;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 21 VLAQLDA 27
b 598 VLAQLDA 604

J. Mol. Biol. 199:373-377(1988).
[2]
RN SEQUENCE FROM N.A.
RP Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
RA Mesyanzhinov V., Ruger W., Sidham T., Thomas E.;
RT "Bacteriophage T4 genome analysis.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=98240730; PubMed=9560385;
RA Wang F.J., Ripley L.S.;
RT "The spectrum of acridine resistant mutants of bacteriophage T4
RT reveals cryptic effects of the tBL14 DNA polymerase allele on
RT spontaneous mutagenesis.";
RL Genetics 148:1655-1665(1998).
CC -!- FUNCTION: Mutations in the ac gene confer resistance to acridine-
CC inhibition of phage development.
CC -----
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CC -----
CC EMBL; AF158101; RAD42488.1; --
DR FIR; S01870; S01870.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; UNKNOWN_1.
KW Antibiotic resistance.
SQ SEQUENCE 51 AA; 5472 MW; 63FDCB0161A8B569 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 ACVLTI 102
Db 18 ACVLTI 23

RESULT 15
D230_PEA STANDARD; PRT; 72 AA.
ID D230_PEA
AC Q01783;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Disease resistance response protein 230 precursor.
GN F1230.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Alaska;
RX MEDLINE=92190628; PubMed=1799696;
RA Chiang C.C., Hadwiger L.A.;
RT "The Fusarium solani-induced expression of a pea gene family encoding
RT high cysteine content proteins.";
RL Mol. Plant Microbe Interact. 4:324-331(1991).
CC -!- INDUCTION: UPON CONTACT WITH THE PLANT PATHOGEN FUNGUS FUSARIUM
CC SOLANI.
CC -!- PTM: FOUR DISULFIDE BONDS MAY BE PRESENT.
CC -!- SIMILARITY: BELONGS TO THE PLANT DEFENSIN FAMILY.
CC -----
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CC -----
DR EMBL; L01578; AAA79117.1; -.
DR PIR; T06599; T06599.
DR InterPro; IPR002118; Gamma-thionin.
DR InterPro; IPR003614; Kntc1.
DR Pfam; PF00304; gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; Kntc1; 1.
KW Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 72 DISEASE RESISTANCE RESPONSE PROTEIN 230.
SQ SEQUENCE 72 AA; 7986 MW; 50B6A90E5FE0CE2B CRC64;

Query Match 4.9%; Score 6; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 43; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLL 10
DB 8 CLSFLL 13

RESULT 16
R28A MYCTU STANDARD; PRT; 94 AA.
AC Q10879;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L28-1.
GN RPB1 OR RPB OR RV0105C OR MT0114 OR MTCY251.24C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala P.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----

DR EMBL; 274410; CAA98918.1; -.
DR EMBL; AE006923; AAK44336.1; -.
DR PIR; A70752; A70752.
DR TIGR; MT0114; -.
DR TubercuList; RV0105C; -.
DR HAMAP; MF_00373; -.
DR InterPro; IPR001383; Ribosomal_L28.
DR Pfam; PF00830; Ribosomal_L28; 1.
DR TIGRFAMs; TIGR00009; L28; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 94 AA; 10530 MW; D2D927D1934C83F7 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RAGSAP 65
DB 72 RAGSAP 77

RESULT 17
H1C2 TRYCR STANDARD; PRT; 97 AA.
AC P40268;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Histone H1.C2.
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
CX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tulaneu 2;
RX MEDLINE=95059220; PubMed=7969272;
RA Aaslund L., Carlsson L., Henriksson J., Rydaaker M., Toro G.C.,
RA Galanti N., Pettersson U.;
RT "A gene family encoding heterogeneous histone H1 proteins in
RT Trypanosoma cruzi";
RL Mol. Biochem. Parasitol. 65:317-330(1994).
CC -----
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CC -----
DR EMBL; L27115; AAA66478.1; -.
DR Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SQ SEQUENCE 97 AA; 10290 MW; AA8073FDBA36121B CRC64;

Query Match 4.9%; Score 6; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LSCVLS 43
DB 8 LSCVLS 13

RESULT 18
VE7 HPV35 STANDARD; PRT; 99 AA.
AC P27230;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE E7 protein.
GN E7.
OS Human papillomavirus type 35.


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DR      InterPro; IPR003006; Ig_MHC.
DDR     InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
KW      Immunoglobulin V region; Signal; Hybridoma.
FT      NON_TER 1
FT      SIGNAL <1 4
FT      CHAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.
FT      DISULFID 27 93 BY SIMILARITY.
FT      NON_TER 100 100
FT      SEQUENCE 100 AA; 10729 MW; 5D9AF363C5C2632F CRC64;
SQ
Query Match 4.9%; Score 6; DB 1; Length 100;
Best Local Similarity 100.0%; Pred.No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 IPDRFS 88
DB      63 IPDRFS 68

RESULT 20
KV3A_HUMAN
ID      KV3A_HUMAN STANDARD; PRT; 108 AA.
AC      P01619;
DT      21-JUL-1986 (Rel. 01, Created)
DD      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1986 (Rel. 38, Last annotation update)
DD      15-JUL-1986 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-III region B6.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
RN      [1]
RP      SEQUENCE.
RA      Milstein C.;
RT      "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, Fr4 and B6.";
RL      FEBS Lett. 2:301-304(1969).
PI      MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR      LIR; A01891; K3HUB6.
DR      HSSP; P80362; 1WTL.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
KW      Immunoglobulin V region; Bence-Jones protein.
FT      DISULFID 23 89 BY SIMILARITY.
FT      NON_TER 108 108
FT      SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;
SQ
Query Match 4.9%; Score 6; DB 1; Length 108;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 IPDRFS 88
DB      59 IPDRFS 64

RESULT 21
LV3A_HUMAN
ID      LV3A_HUMAN STANDARD; PRT; 108 AA.
AC      P01714;
DT      21-JUL-1986 (Rel. 01, Created)
DD      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Ig lambda chain V-III region SH.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE.
MEDLINE=70166723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein. 3. The
complete amino acid sequence and the location of the disulfide
bridges."
J. Biol. Chem. 245:2171-2176(1970).
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR: A01980; L3HUSH.
HSSP; P80748; 2LOI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-LIKE.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; IG; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
IMMUNOGLOBULIN V region; Bence-Jones protein.
DOMAIN 1 97
IG-LIKE.
NON TER 108 108
DISULFID 21 86
SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 83 IPDRFS 88
|||||
56 IPDRFS 61

RESULT 22
KV3E HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE.
MEDLINE=82046598; PubMed=6794615;
Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
group."
Biochemistry 20:5816-5822(1981).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
PIR; A01892; K3HUSI.
HSSP; P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-LIKE.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; IG; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
IMMUNOGLOBULIN V region.
DISULFID 23 89
BY SIMILARITY.

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FT NON TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
59 IPDRFS 64

Db 59 IPDRFS 64

RESULT 23
KV3D HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE.
MEDLINE=72188439; PubMed=5027703;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production."
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01895; K3HUTI.
HSSP; P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-LIKE.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; IG; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
IMMUNOGLOBULIN V region; Bence-Jones protein.
DISULFID 23 89
BY SIMILARITY.
NON TER 109 109
SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;
Query Match 4.9%; Score 6; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
|||||
59 IPDRFS 64

Db 59 IPDRFS 64

RESULT 24
KV3E HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]

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P SEQUENCE.
X MEDLINE=82046598; PubMed=6794615;
A Andrews D.W., Capra J.D.;
T "Amino acid sequence of the variable regions of light chains from two
I idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
T Group";
L Biochemistry 20:5816-5822(1981).
C -I- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
C GLOBULIN ACTIVITY.
R PIR; A01896; K3HUWL.
R HSP; P80362; LWL.
R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0003823; F:antigen binding activity; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; IG-LIKE.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; IG; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS50835; IG_LIKE; 1.
W Immunoglobulin V region.
T DISULFID 23 89
T NON TER 109 109 BY SIMILARITY.
T Q SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 4.9%; Score 6; DB 1; Length 109;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 83 IPDRFS 88
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b 59 IPDRFS 64

RESULT 25
Y3G HUMAN STANDARD; PRT; 109 AA.
C P04206;
T 20-MAR-1987 (Rel. 04, Created)
T 20-MAR-1987 (Rel. 04, Last sequence update)
T 15-JUL-1999 (Rel. 38, Last annotation update)
T IG kappa chain V-II region GOL (Rheumatoid factor).
R Homo sapiens (Human).
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
[1]

SEQUENCE.
X MEDLINE=82630578; PubMed=3085710;
X Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
X "Amino acid sequence of a light chain variable region of a human
X rheumatoid factor of the Wa idiotype group, in part predicted by its
X reactivity with antipeptide antibodies";
X Mol. Immunol. 23:239-244(1986).
X PIR; A01893; K3HUGO.
X HSP; P80362; LWL.
X GO; GO:0005576; C:extracellular; NAS.
X GO; GO:0003823; F:antigen binding activity; NAS.
X GO; GO:0006955; P:immune response; NAS.
X InterPro; IPR007110; IG-LIKE.
X InterPro; IPR003006; IG_MHC.
X InterPro; IPR003596; IG_V.
X Pfam; PF00047; IGV; 1.
X SMART; SM00406; IGV; 1.
X PROSITE; PS50835; IG_LIKE; 1.
W Immunoglobulin V region.
T DISULFID 23 89
T NON TER 109 109 BY SIMILARITY.
T Q SEQUENCE 109 AA; 11830 MW; 9349A5B1D9358B86 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 109;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
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Db 59 IPDRFS 64

RESULT 26
LV2E HUMAN STANDARD; PRT; 109 AA.
ID LV2E HUMAN
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-I region EPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86000126; PubMed=3929803;
RA Toft K.G., Sletten K., Husby G.;
RT "The amino-acid sequence of the variable region of a carbohydrate-
RT containing amyloid fibril protein EPS (immunoglobulin light chain,
RT type lambda).";
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC -I- MISCELLANEOUS; RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
CC PEPTIDES WERE POSITIONED BY HOMOLOGY.
CC -I- SIMILARITY; Contains 1 immunoglobulin-like domain.
DR PIR; A24656; LIHURP.

DR HSP; P01703; 7FAP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid; Glycoprotein.
FT DOMAIN 1 105 IG-LIKE
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .).
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24DSAC73 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 109;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
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Db 59 IPDRFS 64

RESULT 27
LV2E HUMAN STANDARD; PRT; 109 AA.
ID LV2E HUMAN
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80006606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human IgA1 immunoglobulin. V. Amino acid

T sequence of a human IgA lambda light chain (Bur).";
L J. Biol. Chem. 254:9006-9016(1979).
C -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN- AND MCG-
C MARKERS.
C -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
R PIR; A01974; L2HUBR.
R HSP; P01709; 2MCG.
R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0003823; F:antigen binding activity; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; IG-like.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; IG; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS0835; IG LIKE; 1.
R Immunoglobulin V region; Pyrrolidone carboxylic acid.
T DOMAIN 1 106
T MOD RES 1 1
T DISULFID 22 90
T SITE 91 91
T APPEARS TO BE A FREE BUT UNREACTIVE
T SULFHYDRYL GROUP.
T NON TER 109
T SEQUENCE 109 AA; 11506 MW; BFD8AE1C5D267FAB CRC64;

Query Match 4.9%; Score 6; DB 1; Length 109;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2y 54 VSWYQQ 59
35 VSWYQQ 40

RESULT 28
LV2J HUMAN STANDARD; PRT; 110 AA.
AC P01713; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region NIG-58.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 4.9%; Score 6; DB 1; Length 109;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2y 54 VSWYQQ 59
35 VSWYQQ 40

RESULT 29
LV2J HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2y 54 VSWYQQ 59
35 VSWYQQ 40

RESULT 30
LV2A HUMAN STANDARD; PRT; 111 AA.
AC P01704;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region TOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 4.9%; Score 6; DB 1; Length 110;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 54 VSWYQQ 59
Db 35 VSWYQQ 40

RESULT 29
LV2D HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 54 VSWYQQ 59
Db 34 VSWYQQ 39

RESULT 30
LV2A HUMAN STANDARD; PRT; 111 AA.
AC P01704;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region TOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

A Nabeshima Y., Ikenaka T.;
I "Primary structure of cryo Bence-Jones protein (Tog) from the urine
of a patient with IgD myeloma";
L Mol. Immunol. 16:439-444(1979).
C -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
R R PIR; A01969; L2HUTG.
R R HSSP; P01709; 2MCG.
R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0003823; F:antigen binding activity; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; IG-LIKE.
R InterPro; IPR003006; IG_MHC.
R Pfam; PF00047; IG; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS0835; IG_LIKE; 1.
W Immunoglobulin V region; Bence-Jones protein;
W Pyrrrolidone carboxylic acid.
T DOMAIN 1 100 IG-LIKE.
T MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
T DISULFID 22 90 BY SIMILARITY.
T NON_TER 111 111
Q SEQUENCE 111 AA; 11713 MW; FD20AEF4CE5364E2 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 54 VSWYQQ 59
b 35 VSWYQQ 40

RESULT 31
V2B HUMAN STANDARD; PRT; 111 AA.
C P01705;
T 21-JUL-1986 (Rel. 01, Created)
T 21-JUL-1986 (Rel. 01, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
E Ig lambda chain V-II region NEI.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE.
X MEDLINE=7223323; PubMed=5043326;
A Garver F.A., Hilschmann N.;
T "The primary structure of a monoclonal human lambda-type
immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
L Eur. J. Biochem. 26:10-32(1972).
C -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
R R PIR; A01970; L2HUNI.
R R HSSP; P01709; 2MCG.
R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0003823; F:antigen binding activity; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; IG-LIKE.
R InterPro; IPR003006; IG_MHC.
R Pfam; PF00047; IG; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS0835; IG_LIKE; 1.
W Immunoglobulin V region; Bence-Jones protein; Glycoprotein;
W Pyrrrolidone carboxylic acid.
T DOMAIN 1 106 IG-LIKE.
T MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
T DISULFID 22 90 BY SIMILARITY.
T CARBOHYD 96 96 N-LINKED (GLCNAC. . .).
T NON_TER 111 111

SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59
DB 35 VSWYQQ 40

RESULT 32
LV2C HUMAN STANDARD; PRT; 111 AA.
ID LV2C_HUMAN
AC P01706;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region BOH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75115478; PubMed=804002;
RA Kohler H., Rudofsky S., Klusens L.;
RT "The primary structure of a human lambda II chain.";
RL J. Immunol. 114:415-421(1975).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE O2+ MARKER.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01972; L2HUBH.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrrolidone carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11650 MW; 94520309932623B8 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59
DB 35 VSWYQQ 40

RESULT 33
LV2D HUMAN STANDARD; PRT; 111 AA.
ID LV2D_HUMAN
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region TRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

XX MEDLINE=80114123; PubMed=118915;
YA Scholz R., Yang C., Hilschmann N.;
IT "Rule of antibody structure. Primary structure of a human monoclonal
IT IgA1-immunoglobulin (myeloma protein tro). VI. Amino acid sequence of
YT the L-chain, lambda-type, subgroup II.";
YL Hoppe-Seyler's Z. Physik. Chem. 360:1903-1918(1979).
XC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
XC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01973; L2HUTR.
DR HSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 106
FT MOD_RES 1 1
FT DISULFID 22 90
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11561 MW; 99DC457A12B8F6E1 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 54 VSWYQQ 59
Db 35 VSWYQQ 40
|||||

RESULT 34
LV2F HUMAN
ID LV2F HUMAN STANDARD; PRT; 111 AA.
AC P01709;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region MCG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=75013804; PubMed=4415202;
RA Fett J.W., Deutsch H.F.;
RT "Primary structure of the Mcg lambda chain."
RL Biochemistry 13:4102-4114(1974).
RN [2]
RP LAMBDA CHAIN GENES.
RX MEDLINE=76093781; PubMed=812801;
RA Fett J.W., Deutsch H.F.;
RT "A new lambda-chain gene."
RL Immunochimistry 12:643-652(1975).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA Panagiotopoulos N.;
RT "Rotational alignment and divergent evolution of domains in
RT immunoglobulin light chains."
RL Biochemistry 14:3953-3961(1975).
RN [4]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=90133913; PubMed=2515285;
RA Ely K.R., Herron J.N., Harter M., Edmundson A.B.;
RT "Three-dimensional structure of a light chain dimer crystallized in
RT water. Conformational flexibility of a molecule in two crystal
RT forms."

J. Mol. Biol. 210:601-615(1989).
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
-!- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
CC A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
CC SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC MARKERS.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90381; L2HUMC.
DR PDB; 2MCG; 15-JUL-92.
DR PDB; 1A8J; 17-JUN-98.
DR PDB; 1DCL; 15-MAY-97.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure;
KW Pyrrolidone carboxylic acid. IG-LIKE.
FT DOMAIN 1 108
FT MOD_RES 1 1
FT DISULFID 22 90
FT STRAND 5 5
FT STRAND 10 12
FT STRAND 18 23
FT TURN 26 32
FT STRAND 36 40
FT TURN 42 43
FT STRAND 50 51
FT TURN 52 54
FT STRAND 55 55
FT TURN 62 63
FT STRAND 66 68
FT STRAND 72 77
FT HELIX 82 84
FT STRAND 86 93
FT STRAND 99 101
FT STRAND 105 109
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11558 MW; 7CC1D6E2FA3377BA CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59
Db 35 VSWYQQ 40
|||||

RESULT 35
LV2G HUMAN
ID LV2G HUMAN STANDARD; PRT; 111 AA.
AC P01710;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region BO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71103825; PubMed=5532228;
RA Wikler M., Putnam F.W.;
RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
RT chymotryptic peptides, and sequence of protein Bo."
J. Biol. Chem. 245:4488-4507(1970).

C -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
R PIR; A01976; L2HUBO.
R HSSP; P01709; 2MCG.
R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0003823; F:antigen binding activity; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; IG-LIKE.
R InterPro; IPR003006; IG-MHC.
R InterPro; IPR003596; IG-V.
R Pfam; PF00047; IG; 1.
R SMART; SMO0406; IGV; 1.
R PROSITE; PS50835; IG-LIKE; 1.
W Immunoglobulin V region; Bence-Jones protein;
W Pyridolone carboxylic acid.
T DOMAIN 1 106 IG-LIKE.
T MOD_RES 1 106 PYRROLIDONE CARBOXYLIC ACID.
T DISULFID 22 90 BY SIMILARITY.
T NON_TER 111 111
Q SEQUENCE 111 AA; 11785 MW; 925FA1BF72421BAC CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 54 VSWYQQ 59
| | | | |
b 35 VSWYQQ 40

RESULT 36
V2H HUMAN
D -LV2H HUMAN STANDARD; PRT; 111 AA.
C P01711;
T 21-JUL-1986 (Rel. 01, Created)
T 21-JUL-1986 (Rel. 01, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
E IG lambda chain V-II region VII.
S Homo sapiens (Human)
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE.
X MEDLINE=71215142; PubMed=5087637;
A Bonstingl H., Hilschmann N.;
T "Structural rule of antibodies. Complete primary structure of a
monoclonal immunoglobulin L chain of the lambda type, subgroup II
(Bence Jones protein VII).";
T Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).
C -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
R PIR; A01977; L2HUVL.
R HSSP; P01709; 2MCG.
R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0003823; F:antigen binding activity; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; IG-LIKE.
R InterPro; IPR003006; IG-MHC.
R InterPro; IPR003596; IG-V.
R Pfam; PF00047; IG; 1.
R SMART; SMO0406; IGV; 1.
R PROSITE; PS50835; IG-LIKE; 1.
W Immunoglobulin V region; Bence-Jones protein.
T DOMAIN 1 100 IG-LIKE.
T DISULFID 22 90 BY SIMILARITY.
T NON_TER 111 111
Q SEQUENCE 111 AA; 11445 MW; 3913736B3EF367E0 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 ADYICS 116
| | | | |
Db 86 ADYICS 91

RESULT 37
LV2I HUMAN
ID -LV2I HUMAN STANDARD; PRT; 111 AA.
AC P01712;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-II region WIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE.
RX MEDLINE=79062503; PubMed=102365;
RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
RT "Amino acid sequence of the human myeloma lambda chain Win.";
RL Biochim. Biophys. Acta 537:9-21(1978).
CC -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01978; L2HUVN.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyridolone carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD_RES 1 90 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11694 MW; 8C3CE95FE721B87C CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59
| | | | |
Db 35 VSWYQQ 40

RESULT 38
LV2L HUMAN
ID -LV2L HUMAN STANDARD; PRT; 111 AA.
AC P00422;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG gamma lambda chain V-II region DOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE.
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Ballotti V., Negri A., Merlini G., Garver F., Ferrini G.;
RT "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR Immunoglobulin V region.
DR DOMAIN 1 106 IG-LIKE.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11787 MW; F358B1EA2CD7109A CRC64;
Query Match 4.9%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2Y 54 VSWYQQ 59
DB 35 VSWYQQ 40
RESULT 39
LV1H HUMAN
ID LV1H HUMAN STANDARD; PRT; 112 AA.
AC P06867;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=85257662; PubMed=2410269;
RX Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
physicochemical and antigenic features";
RL Eur. J. Biochem. 150:349-357(1985).
CC -!- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
WERE POSITIONED BY HOMOLGY.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
MARKERS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A25479; LIHUM.
DR HSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR Immunoglobulin V region; Monoclonal antibody;
KW Pyridoxine carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD_RES 1 1 PYRIDOXINE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFFB4 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 84 PDRFSA 89

Db 61 PDRFSA 66
RESULT 40
LV2K HUMAN
ID LV2K HUMAN STANDARD; PRT; 112 AA.
AC P04209;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region NTG-84.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=85204383; PubMed=3922791;
RX Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT "Amino acid sequence of an amyloidogenic Bence Jones protein in
myeloma-associated systemic amyloidosis";
RL FEBS Lett. 185:139-141(1985).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01971; L2HUNG.
DR HSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT DOMAIN 1 102 IG-LIKE.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 11581 MW; 988FEF363AE1E4F3 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 VSWYQQ 59
DB 35 VSWYQQ 40
RESULT 41
RNPA COXBU
ID RNPA COXBU STANDARD; PRT; 121 AA.
AC P45648;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribonuclease P protein component (EC 3.1.26.5) (RNasep protein) (RNase
P protein) (Protein C5).
GN RNPA OR CBU1918.
OS Coxiella burnetii.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
CC Coxiellaceae; Coxiella.
CX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I / Bratislava;
RX MEDLINE=94350801; PubMed=8071197;
RA Suhan M., Chen S.Y., Thompson H.A., Hoover T.A., Hill A.,
RA Williams J.C.;
RT "Cloning and characterization of an autonomous replication sequence

T from Coccidia burnettii";
 L J. Bacteriol. 176:5233-5243 (1994).
 N [2]
 P SEQUENCE FROM N.A.
 C STRAIN=Nine Mile Phase I / RSA 493;
 X MEDLINE=2260857; PubMed=12704232;
 A Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
 A Nelson W.C., Ward N.L., Tetelin H., Davidson T.M., Beanan M.J.,
 A DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
 A Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
 A Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
 I "Complete genome sequence of the Q-fever pathogen, Coccidia
 burnettii";
 L Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460 (2003).
 C -i- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence
 from pre-tRNA to produce the mature 5'-terminus. It can also
 cleave other RNA substrates such as 4.5S RNA. The protein
 component plays an auxiliary but essential role in vivo by binding
 to the 5'-leader sequence and broadening the substrate specificity
 of the ribozyme (By similarity).
 C -i- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
 extra-nucleotide from tRNA precursor.
 C -i- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
 protein subunit (By similarity).
 C -i- SIMILARITY: BELONGS TO THE RNPA FAMILY.
 C -----
 C This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 C -----
 R EMBL; U10529; AAA56917.1; -;
 R EMBL; AE016966; AAC91409.1; -;
 R PIR; I40652; I40652.
 R TIGR; CBUL1918; -;
 R HAWAP; MF_00227; -; 1.
 R InterPro; IPR000100; Ribonuclease_P.
 R Pfam; PF00825; Ribonuclease_P; 1.
 R ProDom; PD003629; Ribonuclease_P; 1.
 R TIGRPFAMs; TIGR00189; rnpA; 1.
 R PROSITE; PS00648; RIBONUCLEASE_P; 1.
 Q Hydrolase; Nuclease; Endonuclease; tRNA processing; RNA-binding.
 Q SEQUENCE 121 AA; 14398 MW; E9402C53D208EFC CRC64;

 Query Match 4.9%; Score 6; DB 1; Length 121;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 67 YLLYR 72
 |||||
 32 YLLYR 37

RX MEDLINE=99121216; PubMed=9920759;
 RA Liu H.T., Wang Y.G., Zhang Y.M., Song Q.S., Di C.H., Chen G., Tang J.,
 RA Ma D.L.;
 RT "TFAR19, a novel apoptosis-related gene cloned from human leukemia
 cell line TF-1, could enhance apoptosis of some tumor cells induced
 by growth factor withdrawal";
 RT Biochem. Biophys. Res. Commun. 254:203-210 (1999).
 RL -i- FUNCTION: MAY FUNCTION IN THE PROCESS OF APOPTOSIS (BY
 CC SIMILARITY).
 CC -i- TISSUE SPECIFICITY: Widely expressed.
 CC -i- SIMILARITY: BELONGS TO THE PDCD5 FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 C -----
 DR EMBL; AF161074; AAD45607.1; -;
 DR HSSP; O27652; 1E1J.
 DR MGD; MGI:1913538; Pcd5.
 DR InterPro; IPR002836; TFAR19-related.
 DR Pfam; PF01984; dsDNA bind; 1.
 DR ProDom; PD008148; TFAR19-related; 1.
 KW Apoptosis.
 SQ SEQUENCE 126 AA; 14275 MW; 05796820CD5C780B CRC64;

 Query Match 4.9%; Score 6; DB 1; Length 126;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 108 EDDADY 113
 |||||
 121 EDDADY 126

RESULT 43
 KV3K HUMAN
 ID KV3K HUMAN STANDARD; PRT; 128 AA.
 AC P06311;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region IARC/BL41 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041852; PubMed=2997711;
 RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 RT III";
 RL Nucleic Acids Res. 13:6499-6513 (1985).
 CC -----
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 C -----
 DR EMBL; Z00021; CAA77316.1; -;
 DR PIR; A01899; K3HU41.
 DR HSSP; P01607; 1REI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
FT CHAIN 1 20 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 128 FRAMEWORK-1.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957FOFE3B9012 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 83 IPDRFS 88
DB 78 IPDRFS 83

RESULT 44

KV3M HUMAN
ID KV3M HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J.; Tomhave E.; Chen P.P.; Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
LEUKEMIA.
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.

DR PIR; P10022; K3HUHA.
DR HSP; P80362; 1WT.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
FT CHAIN 1 20 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 129 FRAMEWORK-1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 55 FRAMEWORK-2.
FT DOMAIN 56 70 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 71 77 FRAMEWORK-3.
FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 110 118 JK1 SEGMENT.
FT DOMAIN 119 129 BY SIMILARITY.
FT DISULFID 43 109

FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 83 IPDRFS 88
DB 79 IPDRFS 84

RESULT 45

KV3M HUMAN
ID KV3M HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J.; Tomhave E.; Chen P.P.; Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
LEUKEMIA.
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.

DR PIR; P10021; K3HUHI.
DR HSP; P80362; 1WT.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
FT CHAIN 1 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 129 FRAMEWORK-1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 55 FRAMEWORK-2.
FT DOMAIN 56 70 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 71 77 FRAMEWORK-3.
FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 110 118 JK1 SEGMENT.
FT DOMAIN 119 129 BY SIMILARITY.
FT DISULFID 43 109
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 83 IPDRFS 88
DB 79 IPDRFS 84

RESULT 46

LVIG HUMAN
ID LVIG HUMAN STANDARD; PRT; 130 AA.
AC P06316;

```

Query Match          4.9%; Score 6; DB 1; Length 130;
Best Local Similarity 100.0%; Pred.No.71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

          54 VSWYQQ 59
          |||||
          53 VSWYQQ 58

RESULT 47
RV5B MOUSE
KV5B MOUSE STANDARD; PRT; 136 AA.
C P01634;
T 21-JUL-1986 (Rel. 01, Created)
T 21-JUL-1986 (Rel. 01, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG kappa chain V-V region MOPC 21 precursor.
DS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CC NCBI_TaxID=10090;
CC [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RT Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).

```

QY	54 VSWYQQ	59
Db	62 VSWYQQ	67


```

RESULT 48
VPRI_MOUSE
ID    VPRI_MOUSE   STANDARD;      PRT;       142 AA.
AC    P13372;
DT    01-JAN-1990 (Rel. 13, Created)
DT    01-JAN-1990 (Rel. 13, Last sequence update)
DT    15-SEP-2003 (Rel. 42, Last annotation update)
DE    Immunoglobulin iota chain precursor (VPREB1 protein).
DE    VPREB1.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RX    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=C57BL/6 X DBA/2J;
RX    MEDLINE=8802315; PubMed=3117530;
RA    Kudo A., Melchers F.;
RT    "A second gene, VpreB in the lambda 5 locus of the mouse, which
RT    appears to be selectively expressed in pre-B lymphocytes." ;
RL    EMBO J. 6:2267-2272(1987).
CC    -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC    COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC    COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC    STEPS OF B-CELL DIFFERENTIATION.
CC    -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC    -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
```

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EMBL; X05556; CAA29071.1; -
PIR; A28344; A28344.
HSSP; P01607; IREI.
MGD; MGI:98936; Vpreb1.
GO; GO:0005886; C:plasma membrane; IPI.
GO; GO:0004872; P:receptor activity; IPI.
GO; GO:0030097; P:hemopectasis; IMP.
GO; GO:0006955; P:immune response; IPI.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
Pfam; PF00047; IG_1.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin domain; B-cell; Signal.
CHAIN 1 19
DOMAIN 20 41
DOMAIN 42 56
DOMAIN 57 70
DOMAIN 71 81
DOMAIN 82 115
DISULFID 41 115
SEQUENCE 142 AA; 16125 MW; 2E1B5F963A0F448C CRC64;
Query Match 4.9%; Score 6; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 38 LSCTLS 43
39 LSCTLS 44

RESULT 49
VPR2 MOUSE
ID VPR2 MOUSE STANDARD; PRT; 142 AA.
AC P13373;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Immunoglobulin omega chain precursor (VpreB2 protein).
GN VPREB2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2J;
RX MEDLINE=88029315; PubMed=3117530;
RA Kudo A., Melchers F.
RT "A second gene, VpreB in the lambda 5 locus of the mouse, which
appears to be selectively expressed in pre-B lymphocytes."
RL EMBO J. 6:2267-2272(1987).
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
STEPS OF B-CELL DIFFERENTIATION.
CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

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EMBL; X05563; CAA29077.1; -
PIR; B28344; B28344.
HSSP; P01607; IREI.
MGD; MGI:98937; Vpreb2.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
Pfam; PF00047; IG_1.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG LIKE; 1.
Immunoglobulin domain; B-cell; Signal.
CHAIN 1 19
DOMAIN 20 41
DOMAIN 42 56
DOMAIN 57 70
DOMAIN 71 81
DOMAIN 82 115
DISULFID 41 115
SEQUENCE 142 AA; 16052 MW; 7EA7128A4E63D920 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LSCTLS 43
39 LSCTLS 44

RESULT 50
RST1 AVESA
ID RST1 AVESA STANDARD; PRT; 169 AA.
AC P50695;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thaumatin-like pathogenesis-related protein 1 precursor.
GN RASTL-1.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Avenae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Rodney;
RX MEDLINE=96303536; PubMed=8755626;
RA Lin K.C., Bushnell W.R., Szabo L.J., Smith A.G.
RT "Isolation and expression of a host response gene family encoding
thaumatin-like proteins in incompatible oat-stem rust fungus
interactions."
RL Mol. Plant Microbe Interact. 9:511-522(1996).
CC -!- FUNCTION: ASSOCIATED WITH RESISTANCE AGAINST STEM RUST FUNGI.
CC -!- SIMILARITY: Belongs to the thaumatin family.

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EMBL; L39774; AAB09224.1; -
HSSP; P33679; 1DU5.

```
R InterPro: IPR001938; Thaumatin.
R Pfam: PF00314; Thaumatin; 1.
R PRINTS; PR00347; THAUMATIN.
R ProDom; PD001321; Thaumatin; 1.
R SMART; SM00205; THN; 1.
R PROSITE; PS00316; THAUMATIN; 1.
W Plant defense; Pathogenesis-related protein; Fungicide;
W Multigene family; Signal.
T SIGNAL 1 21
T CHAIN 22 169
T POTENTIAL.
T THAUMATIN-LIKE PATHOGENESIS-RELATED
T THAUMATIN-LIKE PATHOGENESIS-RELATED
T PROTEIN 1.
Q SEQUENCE 169 AA; 17353 MW; 7377CA770CC2B09D CRC64;

Query Match 4.9%; Score 6; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 38 LSCITLS 43
  |||||
b 90 LSCITLS 95

RESULT 51
RST4_AVEA
ID RST4_AVEA STANDARD; PRT; 169 AA.
AC PS0696;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thaumatin-like pathogenesis-related protein 2 precursor.
DE RASTL-2.
GN Avena sativa (Oat).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Aveneae; Avena.
OC NCBI_TaxID=4498;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Rodney; PubMed=8755626;
RX MEDLINE=96303536;
RA Lin K.C., Bushnell W.R., Szabo L.J., Smith A.G.;
RT "Isolation and expression of a host response gene family encoding
RT thaumatin-like proteins in incompatible oat-stem rust fungus
RT interactions.";
RL Mol. Plant Microbe Interact. 9:511-522(1996).
CC -!- FUNCTION: ASSOCIATED WITH RESISTANCE AGAINST STEM RUST FUNGI.
CC -!- SIMILARITY: Belongs to the thaumatin family.
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CC
CC EMBL; L39775; AAB09225.1; -
CC HSP; P33679; 1DU5
CC InterPro; IPR001938; Thaumatin.
CC Pfam; PF00314; Thaumatin; 1.
CC PRINTS; PR00347; THAUMATIN.
CC ProDom; PD001321; Thaumatin; 1.
CC SMART; SM00205; THN; 1.
CC PROSITE; PS00316; THAUMATIN; 1.
CC Plant defense; Pathogenesis-related protein; Fungicide;
CC Multigene family; Signal.
CC SIGNAL 1 21
CC CHAIN 22 169
CC POTENTIAL.
CC THAUMATIN-LIKE PATHOGENESIS-RELATED
CC PROTEIN 1.
Q SEQUENCE 169 AA; 17403 MW; 0030CE363CCEB79 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 38 LSCITLS 43
  |||||
b 90 LSCITLS 95

RESULT 52
RST3_AVEA
ID RST3_AVEA STANDARD; PRT; 169 AA.
AC PS0697;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thaumatin-like pathogenesis-related protein 3 precursor.
DE RASTL-3.
GN Avena sativa (Oat).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Aveneae; Avena.
OC NCBI_TaxID=4498;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Rodney; PubMed=8755626;
RX MEDLINE=96303536;
RA Lin K.C., Bushnell W.R., Szabo L.J., Smith A.G.;
RT "Isolation and expression of a host response gene family encoding
RT thaumatin-like proteins in incompatible oat-stem rust fungus
RT interactions.";
RL Mol. Plant Microbe Interact. 9:511-522(1996).
CC -!- FUNCTION: ASSOCIATED WITH RESISTANCE AGAINST STEM RUST FUNGI.
CC -!- SIMILARITY: Belongs to the thaumatin family.
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CC
CC EMBL; L39776; AAB09226.1; -
CC HSP; P33679; 1DU5
CC InterPro; IPR001938; Thaumatin.
CC Pfam; PF00314; Thaumatin; 1.
CC PRINTS; PR00347; THAUMATIN.
CC ProDom; PD001321; Thaumatin; 1.
CC SMART; SM00205; THN; 1.
CC PROSITE; PS00316; THAUMATIN; 1.
CC Plant defense; Pathogenesis-related protein; Fungicide;
CC Multigene family; Signal.
CC SIGNAL 1 21
CC CHAIN 22 169
CC POTENTIAL.
CC THAUMATIN-LIKE PATHOGENESIS-RELATED
CC PROTEIN 3.
Q SEQUENCE 169 AA; 17328 MW; 647CA7D5D54108AF CRC64;

Query Match 4.9%; Score 6; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 38 LSCITLS 43
  |||||
b 90 LSCITLS 95

RESULT 53
RST4_AVEA
ID RST4_AVEA STANDARD; PRT; 169 AA.
AC PS0698;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thaumatin-like pathogenesis-related protein 4 precursor.
```


A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
A Leathem S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
A Shimmings M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
T "Genome sequence of *Yersinia pestis*, the causative agent of plague";
L Nature 413:523-527(2001).
N [2]
P SEQUENCE FROM N.A.
X STRAIN=KIMS / Biovar Mediaevalis;
X MEDLINE=22137863; PubMed=12142430;
A Peng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
A Derna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
A Retherson J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
A Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
A Perry R.D.;
T "Genome sequence of *Yersinia pestis* KIM";
L J. Bacteriol. 184:4601-4611(2002).
L - FUNCTION: Protease subunit of a proteasome-like degradation
C complex (By similarity).
C - SUBUNIT: Interacts with hslu (By similarity).
C - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
C - SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B. HSLV SUBFAMILY.
C
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C
R EMBL; AJ414141; CAC89971.1; -;
R EMBL; AE013628; AAM83887.1; -;
R PIR; A10013; A10013.
R MEROPS; T01.006; -;
R HAMAP; MF_00248; -; 1
R InterPro; IPR001353; Protease_protease.
R Pfam; PF00227; protease; 1.
R Hydrolase; Protease; Complete
T INIT MET 0 BY SIMILARITY.
T ACT SITE 1 1 BY SIMILARITY.
T Q SEQUENCE 173 AA; 18763 MW; 4F6DD964BDA75F2C CRC64;
Query Match 4.9%; Score 6; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 105 VQPEDD 110
b 113 VQPEDD 118
RESULT 56
ID VNSC PHODV STANDARD; PRT; 174 AA.
AC P35940;
VT 01-JUN-1994 (Rel. 29, Created)
YT 01-JUN-1994 (Rel. 29, Last sequence update)
YT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Nonstructural protein C.
EN P/V/C.
DC Phocine distemper virus (PDV).
DC Viruses; ssRNA negative-strand viruses; Mononegavirales;
DC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
DX NCBI_TaxID=11240;
RX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=U1ster/88;
RC MEDLINE=92300361; PubMed=1535099;
RA Curran M.D., Rima B.K.;
RT "The genes encoding the phospho- and matrix proteins of phocine
RT distemper virus";
RL J. Gen. Virol. 73:1587-1591(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate DK88-4A;
RC MEDLINE=92341068; PubMed=1634877;
RX Blixenkron-Moeller M., Sharma B., Varsanyi T., Hu A., Norrby E.,
RA Koevamees J.;
RT "Sequence analysis of the genes encoding the nucleocapsid protein and
RT phosphoprotein (P) of phocid distemper virus, and editing of the P
RT gene transcript";
RL J. Gen. Virol. 73:885-893(1992).
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CC
DR EMBL; D10371; BAA01204.1; -;
DR EMBL; X75960; CAA53574.1; -;
DR PIR; JQ1611; JQ1564.
DR InterPro; IPR003875; Paramyxovir_NSC.
DR Pfam; PF02725; Paramyxo_NS_C; 1.
RW Nonstructural protein.
KW CONFLICT 26 26 A -> V (IN REF. 2).
SQ SEQUENCE 174 AA; 20321 MW; A25FF482E94C3A43 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 VSWYQQ 59
Db 121 VSWYQQ 126
RESULT 57
ID TLP-ORISA STANDARD; PRT; 177 AA.
AC P31110;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thaumatin-like protein precursor.
DE Oryza sativa (Rice)
OS Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Nohrin;
RX MEDLINE=94143469; PubMed=8310049;
RA Reimann C., Dudler R.;
RT "cDNA cloning and sequence analysis of a pathogen-induced
RT thaumatin-like protein from rice (*Oryza sativa*)";
RL Plant Physiol. 101:1113-1114(1993).
CC - SUBCELLULAR LOCATION: Secreted (Potential).
CC - INDUCTION: By pathogen infection.
CC - SIMILARITY: Belongs to the thaumatin family.
CC
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CC
DR EMBL; X68197; CAA48278.1; -;
DR PIR; S25551; S25551.
DR HSSP; P33679; 1DU5.
DR Gramene; P31110; -;

JR InterPro; IPR001938; Thaumatin.
JR Pfam; PF00314; Thaumatin; 1.
JR PRINTS; PR00347; THAUMATIN.
JR ProDom; PD001321; Thaumatin; 1.
JR SMART; SM0205; TEN; 1.
JR PROSITE; PS00316; THAUMATIN; 1.
KW SIGNAL. 1 26 POTENTIAL. THAUMATIN-LIKE PROTEIN.
FT CHAIN 27 177
SQ SEQUENCE 177 AA; 17992 MW; 7BA9BC9AE07AA9FF CRC64;

Query Match 4.9%; Score 6; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 38 LSCTLS 43
DB 96 LSCTLS 101

RESULT 58
CYOC_BUCAP STANDARD; PRT; 189 AA.
ID CYOC_BUCAP
AC Q8K995;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-).
GN CYOC OR BUSG454.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamas I., Klason L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Anderson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria."
RL Science 296:2376-2379(2002).
CC -!- FUNCTION: Cytochrome O terminal oxidase complex is the component
CC of the aerobic respiratory chain that predominates when cells are
CC grown at high aeration (By similarity).
CC -!- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubimionone-8 + H(2)O.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 3 family.
CC
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CC
CC EMBL; AB014121; AA67997.1; -
CC InterPro; IPR000298; Cytochrome_oxidase_III.
CC Pfam; PF00510; COX3; 1.
CC ProDom; PD000382; Cytochrome_oxidase_III; 1.
CC PROSITE; PS02533; COX3; 1.
KW Oxidoreductase; Electron transport; Transmembrane; Complete proteome.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 POTENTIAL.
FT DOMAIN 32 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 73 POTENTIAL.
FT DOMAIN 74 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 POTENTIAL.
FT DOMAIN 103 122 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 123 143 POTENTIAL.
FT DOMAIN 144 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 182 POTENTIAL.
FT DOMAIN 183 189 EXTRACELLULAR (POTENTIAL).
SQ SEQUENCE 189 AA; 22162 MW; 1513BB6C59CF558 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LSFLLM 11
DB 95 LSFLLM 100

RESULT 59
APOM_MOUSE STANDARD; PRT; 190 AA.
ID APOM_MOUSE
AC Q9Z1R3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein M (Apo-M) (APOM) (NG20).
GN APOM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Xu N., Dahlbaeck B.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,
RA Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility class III region."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamei M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Probably involved in lipid transport.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY. Highly divergent.
CC
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CC
CC EMBL; AF207820; AAP23407.1; -
CC EMBL; AF109719; AAC82478.1; -

EMBL; AK004530; BAB23349.1; -
MGD; MGI:1930124; Apom.
Transport; Lipid transport; HDL; Signal; Lipocalin.
SIGNAL 1 722 NOT CLEAVED (POTENTIAL).
DISULFID 23 169 POTENTIAL.
DISULFID 95 185 POTENTIAL.
DISULFID 130 159 POTENTIAL.
SEQUENCE 190 AA; 21273 MW; 3D5614DDADF277C4 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
61 AGSAPR 66
75 AGSAPR 80
RESULT 60
POM RAT
D AFOM RAT STANDARD; PRT; 190 AA.
C F14630; Q9QX19;
I 01-AUG-1990 (Rel. 15, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
E 28-FEB-2003 (Rel. 41, Last annotation update)
A Apolipoprotein M precursor (Apo-M) (Apom) (protein P).
V AFOM
S Rattus norvegicus (Rat).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
X NCBI_TaxID=10116;
N SEQUENCE FROM N.A.
P STRAIN=Sprague-Dawley; TISSUE=Liver;
A Xu N.; Dahlbaeck B.;
L Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
P SEQUENCE OF 18-33.
X MEDLINE=90122905; PubMed=2297521;
A Blatter M.-C., James R.W., Borghini I., Martin B.M.,
Hochstrasser A.-C., Pomatta D.;
T "A novel high-density lipoprotein particle and associated protein in
rat plasma";
L Biochim. Biophys. Acta 1042:19-27(1990).
C -1- FUNCTION: Probably involved in lipid transport.
C -1- SUBCELLULAR LOCATION: Secreted. Associated with HDL.
C -1- TISSUE SPECIFICITY: Plasma protein.
C -1- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY. Highly divergent.
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C or send an email to license@isb-sib.ch).
C
C EMBL; AF207821; AAF23408.1; -
R Transport; Lipid transport; HDL; Signal; Lipocalin.
W SIGNAL 1 17
T CHAIN 18 190 APOLIPOPROTEIN M.
T DISULFID 23 169 POTENTIAL.
T DISULFID 95 185 POTENTIAL.
T DISULFID 130 159 POTENTIAL.
T CONFLICT 30 30 M -> T (IN REF. 2).
Q SEQUENCE 190 AA; 21512 MW; E507BD6C202CBBAP CRC64;
Query Match 4.9%; Score 6; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
61 AGSAPR 66
75 AGSAPR 80

Db 75 AGSAPR 80
RESULT 61
I18B MOUSE
ID I18B MOUSE STANDARD; PRT; 191 AA.
AC Q9Z0M9; Q9CUH2; Q9Z0N0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Interleukin-18 binding protein precursor (IL-18BP) (Interferon gamma
DE inducing factor binding protein).
GN IL18BP OR IGIFBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 27-31; 51-54; 92-137;
RP 155-158 AND 162-167.
RC STRAIN=CD-1; TISSUE=Serum;
RX MEDLINE=99192308; PubMed=10094485;
RA Aizawa Y., Akita K., Taniaki M., Korigoe K., Mori T., Nishida Y.,
RA Ushio S., Nakada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.;
RT "Cloning and expression of interleukin-18 binding protein.";
RL FEBS Lett. 445:338-342(1999).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99146382; PubMed=10023777;
RA Novick D., Kim S.H., Pantuzzi G., Reznikov L.L., Dinarello C.A.,
RA Rubinstein M.;
RT "Interleukin-18 binding protein: a novel modulator of the Th1 cytokine
RT response";
RL Immunity 10:127-136(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=99263157; PubMed=10329540;
RA Xiang Y., Moes B.;
RT "Identification of human and mouse homologs of the MCS11-53L-54L
RT family of secreted glycoproteins encoded by the Molluscum contagiosum
RT poxvirus";
RL Virology 257:297-302(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Embryo, Small intestine, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kuchiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pescio G., Quackenbush J.,
RA Schriml L.M., Stauber P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyehaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

```
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S.N., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
T human and mouse cDNA sequences."
T "Generation and initial analysis of more than 15,000 full-length
L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
L -1- FUNCTION: Binds to IL-18 and inhibits its activity. Functions as
C an inhibitor of the early Th1 cytokine response (By similarity).
C -1- SUBCELLULAR LOCATION: Secreted (Potential).
C -1- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=2;
C Names=1;
C IsoId=Q9Z0M9-1; Sequences=Displayed;
C Names=2;
C IsoId=Q9Z0M9-2; Sequences=VSP 002517;
C -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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C -----
C EMBL; AB019505; BAA76375.1; ALT_INIT.
C EMBL; AF110802; AAD17193.1; -.
C EMBL; AF110803; AAD17194.1; -.
C EMBL; AF122907; AAD41052.1; ALT_INIT.
C EMBL; AK009721; BAB26462.1; ALT_INIT.
C EMBL; AK003370; BAB22744.1; ALT_INIT.
C EMBL; AK008452; BAB25677.1; ALT_INIT.
C EMBL; AK009877; BAB26558.1; -.
C EMBL; BC018332; AAH18332.1; ALT_INIT.
C MGD; MG1:1333800; 1118bp.
C GO; GO:0042007; F:interleukin-18 binding activity; ISS.
C GO; GO:0006955; P:immune response; ISS.
C InterPro; IPR007110; Ig-like.
C InterPro; IPR003006; Ig_McC.
C Pfam; PF00047; Ig; 1.
C PROSITE; PS00835; IG_LIKE; 1.
C Immunoglobulin domain; Glycoprotein; Signal; Alternative splicing.
C SIGNAL 1 26
C CHAIN 27 191 INTERLEUKIN-18 BINDING PROTEIN.
C DOMAIN 58 159 IG-LIKE C2-TYPE.
C DISULFID 79 143 BY SIMILARITY.
C CARBOHYD 72 72 N-LINKED (GLNAC. . .) (POTENTIAL).
C CARBOHYD 96 96 N-LINKED (GLNAC. . .) (POTENTIAL).
C CARBOHYD 118 118 N-LINKED (GLNAC. . .) (POTENTIAL).
C CARBOHYD 140 140 N-LINKED (GLNAC. . .) (POTENTIAL).
C VARSPLIC 163 191 DGLTAPPPSQEITLSSHPVSRGAGPVA -> VRLNKEGI
C QGWEERYLKGLEGLAPFPQVPS (in isoform 2).
C /FTID=VSP 002517.
C SEQUENCE 191 AA; 21035 MW; B2F306A30511685B CRC64;
Query Match 4.9%; Score 6; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 PQOVAQ 37
DB 148 PQOVAQ 153
```

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RESULT 62
VG66 BPMD2 STANDARD; PRT; 199 AA.
ID VG66 BPMD2 STANDARD; PRT; 199 AA.
AC O64258;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Gene 66 protein (GP66).
GN 66.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=28369;
RN [1]_TaxID=28369;
RP SEQUENCE FROM N.A.
RA MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: implications for phage
RT evolution."
RL J. Mol. Biol. 279:143-164 (1998).
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CC -----
CC EMBL; AF022214; AAC18507.1; -.
CC FIR; A72808; A72808.
CC InterPro; IPR004843; M-peptidase.
CC Pfam; PF00149; Metallophos; 1.
CC SEQUENCE 199 AA; 22878 MW; 63E20BFD2C5BCAD5 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQDAL 28
DB 59 AQDAL 64
RESULT 63
URK_DEIRA STANDARD; PRT; 210 AA.
AC Q9RXZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Uridine kinase (EC 2.7.1.48) (Uridine monophosphokinase) (Cytidine
DE monophosphokinase).
DE UNK OR DR0159.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]_
RP SEQUENCE FROM N.A.
RA STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
RA MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577 (1999).
```

C -1- CATALYTIC ACTIVITY: ATP + uridine = ADP + UMP.
C -1- CATALYTIC ACTIVITY: ATP + cytidine = ADP + CMP.
C -1- PATHWAY: Pyrimidine Salvage pathway.
C -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
C -1- SIMILARITY: BELONGS TO THE URIDINE KINASE FAMILY.
C
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C
R EMBL, AE001878; AF09747.1; -.
R PIR, E75553; E75553.
R TIGR, DR0159; -.
R HAMAP, MF 00551; -; 1.
R InterPro: IPR006082; PRK.
R InterPro: IPR006083; PRK URK.
R InterPro: IPR000764; Uridine_kin.
R Pfam, PF00485; PRK; 1.
R PRINTS; PR00478; PHRBLKINASE.
R PRINTS; PR00988; URIDINKINASE.
R TIGRFAMs; TIGR00235; udk; 1.
M Transferase; Kinase; ATP-binding; Complete proteome.
M NP BIND 14 ATP (POTENTIAL).
Q SEQUENCE 210 AA; 23660 MW; 1226B9CAD6805882 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 24 QLDALL 29
b 75 QLDALL 80
RESULT 64
RPF SYN3
D TRPF SYN3 STANDARD; PRT; 218 AA.
C P7435;
T 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI).
N TRPF OR SLL0356.
S Synechocystis sp. (strain PCC 6803).
X Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
X NCBI_TaxID=1148;
X [1]
X SEQUENCE FROM N.A.
X MEDLINE=97061201; PubMed=8905231;
X Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
X Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
X Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
X Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
X Yamada M., Yasuda M., Tabata S.;
T "Sequence analysis of the genome of the unicellular cyanobacterium
T Synechocystis sp. strain PCC6803. II. Sequence determination of the
T entire genome and assignment of potential protein-coding regions."
L DNA Res. 3:109-136(1996).
C -1- CATALYTIC ACTIVITY: N-(5-phospho-beta-D-ribose)-anthranilate = 1-
C (2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate.
C -1- PATHWAY: Tryptophan biosynthesis; third step.
C -1- SIMILARITY: BELONGS TO THE TRPF FAMILY.
C
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C
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CC
CC EMBL, D90915; BAA18536.1; -.
CC PIR, S76407; S76407.
CC DR HSSP; O56320; LNSJ.
CC DR HAMAP; MF 00135; -; 1.
CC InterPro: IPR001240; PRAI.
CC Pfam, PF00697; PRAI; 1.
KW Isomerase; Tryptophan biosynthesis; Complete proteome.
SQ SEQUENCE 218 AA; 23881 MW; 37D6035030G55A4F CRC64;
Query Match 4.9%; Score 6; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQLDAL 28
DB 208 AQLDAL 213
RESULT 65
GLNA_DUNSA
ID GLNA_DUNSA STANDARD; PRT; 234 AA.
AC P11600;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
DE (Fragment)
DE Dunaliella salina.
OS Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Dunaliellaceae; Dunaliella.
OX NCBI_TaxID=3046;
RN [1]
RP SEQUENCE FROM N.A.
RA Long Z., Nelson N.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
CC L-glutamine.
CC -1- SUBUNIT: Homooctamer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC
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CC
CC EMBL, X15280; CAA33353.1; -.
CC PIR, S04888; AJDEQ.
CC InterPro: IPR001691; GLN_synth.
CC Pfam, PF00120; Gln-synt; 1.
CC PROSITE; PS00180; GLNA_1; PARTIAL.
CC PROSITE; PS00181; GLNA_ATP; 1.
KW Ligase.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 234 AA; 26224 MW; D5EB25319131DDF6 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 YICSVG 118
DB 38 YICSVG 43
RESULT 66
YMF ECOLI
ID YMF ECOLI STANDARD; PRT; 234 AA.
AC P75968;

15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ymfE.
3N YMF E OR B1138.
3S Escherichia coli.
3C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
3C Enterobacteriaceae; Escherichia.
3X NCBI_TaxID=562;
3N [1]
3P SEQUENCE FROM N.A.
3C STRAIN=K12 / MG1655;
3X MEDLINE=97426617; PubMed=9278503;
3A Blattner F.R., Plunkett G. III, Bloch C.A., Ferna N.T., Burland V.,
3A Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
3A Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
3A Mau B., Shao Y.,
3R "The complete genome sequence of Escherichia coli K-12.";
3L Science 277:1453-1474(1997).
3C -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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3C between the Swiss Institute of Bioinformatics and the EMBL outstation -
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3C or send an email to license@isb-sib.ch).
3C
3C EMBL; AE000214; AAC74222.1; -.
3R PIR; G64858; G64858.
3R EcoGene; SG13449; ymfE.
3C Hypothetical protein; Transmembrane; Complete proteome.
3K TRANSMEM 22 42 POTENTIAL.
3T TRANSMEM 59 79 POTENTIAL.
3T TRANSMEM 154 174 POTENTIAL.
3T TRANSMEM 186 206 POTENTIAL.
3Q SEQUENCE 234 AA; 27578 MW; BAA40C588D285DC2 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 KDEAHN 96
DB 120 KDEAHN 125
RESULT 67
HIS4 RHCOA
ID HIS4 RHCOA STANDARD; PRT; 236 AA.
AC Q30725;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]
DE imidazole-4-carboxamide isomerase (EC 5.3.1.16)
DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
DE isomerase).
GN HIS4
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MT1131;
RC MEDLINE=981132396; PubMed=9473054;
RA Koch H.G., Huang O., Daldal F.;
RT "Isolation and characterization of Rhodobacter capsulatus mutants
RT affected in cytochrome cb3 oxidase activity."
RL J. Bacteriol. 180:969-978(1998).
CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-

phosphoribosylamino)methylideneamino] imidazole-4-carboxamide = 5-
[(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-
phosphoribosyl)imidazole-4-carboxamide.
-1- PATHWAY: Histidine biosynthesis; fourth step.
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: BELONGS TO THE HIS4 / HISF FAMILY.
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EMBL; AF016223; AAC46106.1; -.
HAMAP; MF 01014; -; 1.
DR InterPro; IPR003009; FMN enzyme.
DR InterPro; IPR006063; His4.
DR InterPro; IPR006062; His biosynth.
DR Pfam; PF00977; His biosynth; 1.
DR TIGRFAMs; TIGR00007; TIGR00007; 1.
KW Isomerase; Histidine biosynthesis.
SQ SEQUENCE 236 AA; 24298 MW; 122170D814E9B901 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 FPGQVA 36
DB 120 FPGQVA 125
RESULT 68
SPEH_STRPY
ID SPEH_STRPY STANDARD; PRT; 236 AA.
AC Q9X5C8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Exotoxin type H precursor (SPE H).
GN SPEH OR SPY1008
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M15;
RC MEDLINE=99093428; PubMed=9874566;
RA Proft T., Mofatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes.";
RL J. Exp. Med. 189:189-102(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RC MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar P.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
RC chain.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
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R EMBL; AF124500; AAD30989.1; -;
R EMBL; AB006546; AAK33907.1; -;
R PDB; 1ET9; 24-MAY-00.
R PDB; 1EUA; -;
R InterPro; IPR006123; Staph/Strep toxin.
R InterPro; IPR006126; Staph/Strep tox.
R InterPro; IPR006173; Staph tox OB.
R Pfam; PF02876; Staph_Strip_tox_C; 1.
R Pfam; PF01123; Staph_Strip_toxin; 1.
R PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
R PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
W Toxin; Signal; Complete proteome; 3D-structure.
T CHAIN 1 32 POTENTIAL.
T SIGNAL 33 236 EXOTOXIN TYPE H.
T TAG 33 236
Q SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;

Query Match 4.9%; Score 6; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Y 5 CLSFL 10 STANDARD; PRT; 237 AA.
11111111
b 20 CLSFL 25

RESULT 69

RL HUMAN
D -NRL HUMAN STANDARD; PRT; 237 AA.
C P54845;
Y 01-OCT-1996 (Rel. 34, Created)
Y 01-OCT-1996 (Rel. 34, Last sequence update)
Y 15-SEP-2003 (Rel. 42, Last annotation update)
Y Neural retina-specific leucine zipper protein (NRL) (D14946E).
N NRL.
N Homo sapiens (Human).
N Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
N Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
N NCBI_TaxID=9606;
N [1]
N SEQUENCE FROM N.A.
N TISSUE=Retina;
N MEDLINE=92108034; PubMed=1729696;
N Swaroop A., Xu J.Z., Pawar H., Jackson A.U., Skolnick C., Agarwal N.;
N "A conserved retina-specific gene encodes a basic motif/leucine
N zipper domain.";
N Proc. Natl. Acad. Sci. U.S.A. 89:266-270(1992).
N [2]
N SEQUENCE FROM N.A.
N TISSUE=Retina;
N Jackson A.U., Skolnick C., Swaroop A.;
N Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
N [3]
N SEQUENCE FROM N.A.
N MEDLINE=98008930; PubMed=9344655;
N Farjo O., Jackson A.U., Piek-Dahl S., Scott K., Kimberling W.J.,
N Sieving P.A., Richards J.E., Swaroop A.;
N "Human bzip transcription factor gene NRL: structure, genomic
N sequence, and fine linkage mapping at 14q11.2 and negative mutation
N analysis in patients with retinal degeneration.";
N Genomics 45:395-401(1997).
N [4]
N SEQUENCE FROM N.A.
N TISSUE=Eye;
N MEDLINE=22386257; PubMed=12477932;
N Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
N Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosa S.A., Locuella N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN VARIANT ADPR THR-50.
RX MEDLINE=99206598; PubMed=10192380;
RA Bessant D.A.R., Payne A.M., Mitton K.P., Wang Q.-L., Swain P.K.,
RA Plant C., Bird A.C., Zack D.J., Swaroop A., Bhattacharya S.S.;
RA "A mutation in NRL is associated with autosomal dominant retinitis
RT pigmentosa.";
RL Nat. Genet. 21:355-356(1999).
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- TISSUE SPECIFICITY: NEURAL RETINA.
CC -I- DISEASE: Defects in NRL are a cause of autosomal dominant
CC retinitis pigmentosa (ADRP) [MIM:162080].
CC -I- SIMILARITY: Belongs to the bzip family.
CC -I- DATABASE: NAME-Mutations of the NRL gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/nrlmut.htm".

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EMBL; M95925; AAA96828.1; -;
EMBL; M81840; AAA59948.1; -;
EMBL; U95012; AAB82768.1; -;
EMBL; BC012395; AAH12395.1; -;
PIR; A41796; A41796.
TRANSFAC; T01082;
Genew; HGNC:18002; NRL.
MIM; 162080; -;
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003677; F:DNA binding activity; TAS.
GO; GO:0003704; F:specific RNA polymerase II transcription fa...; TAS.
GO; GO:0007468; P:regulation of rhodopsin gene activity; TAS.
GO; GO:0006366; P:transcription from Pol II promoter; TAS.
GO; GO:0007601; P:vision; TAS.
InterPro; IPR004827; TF_bzip.
Pfam; PF03131; bzip_Maf; 1.
SMART; SM00338; BRLZ; 1.
PROSITE; PS0217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC; FALSE_NEG.
Transcription regulation; DNA-binding; Nuclear protein;
Disease mutation; Retinitis pigmentosa; Vision.
BASIC MOTIF.
DOMAIN 159 185
FT LEUCINE-ZIPPER.
FT DOMAIN 187 208
FT S -> T (in ADRP; increased
FT VARIANT 50 50
FT transactivation activity).
FT /FTID=VAR 009268.
FT
SQ SEQUENCE 237 AA; 25940 MW; CCABEDC1123614 CRC64;

Query Match

4.9%; Score 6; DB 1; Length 237;

```
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 23 AQLDAL 28
b 196 AQLDAL 201

RESULT 70
RL MOUSE
D_NRL_MOUSE STANDARD; PRT; 237 AA.
C P54846;
T 01-OCT-1996 (Rel. 34, Created)
T 01-OCT-1996 (Rel. 34, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Neural retina-specific leucine zipper protein (NRL).
N NRL.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=BALB/c; TISSUE=Retina;
K MEDLINE=94116986; PubMed=8288222;
A Farjo O., Jackson A.U., Xu J., Gryzenia M., Skolnick C.,
A Agarwal N., Swarcop A.;
T "Molecular characterization of the murine neural retina leucine
zipper gene, Nrl."
C Genomics 18:216-222(1993).
C -1- SUBCELLULAR LOCATION: Nuclear.
C -1- TISSUE SPECIFICITY: NEURAL RETINA.
C -1- SIMILARITY: Belongs to the bZIP family.
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C -----
C EMBL: L14935; AAA16843.1;
C PIR: A48912; A48912.
C TRANSFAC; T01438;
C MGD; MGI:102567; Nrl.
C InterPro; IPR004827; TF bZIP.
C InterPro; IPR004826; TF Maf.
C Pfam; PF03131; bZIP Maf; 1.
C SMART; SM00338; BRLZ; 1.
C PROSITE; PS02017; bZIP.
C PROSITE; PS00036; bZIP_BASIC; FALSE_NEG.
K Transcription regulation; DNA-binding; Nuclear protein.
FT DNA BIND 159 185
FT DOMAIN 187 208
FT LEUCINE-ZIPPER.
SQ SEQUENCE 237 AA; 26083 MW; APLA2B372CG5EC8 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDAL 28
Db 196 AQLDAL 201

RESULT 71
UPK THEM A
ID UPK THEM A STANDARD; PRT; 237 AA.
AC Q9WZ25;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```

```
DE Putative undecaprenol kinase (EC 2.7.1.66) (Bacitracin resistance
DE protein).
DE UPK OR BACA OR TW0893.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS8 / DSM 3109;
RX MEDLINE=93287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
Genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
CC -1- FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl
phosphate. Confers resistance to bacitracin (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + undecaprenol = ADP + undecaprenyl
phosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- MISCELLANEOUS: Bacitracin is thought to be involved in inhibition
of peptidoglycan synthesis by sequestering undecaprenyl
diphosphate reducing the pool of lipid carrier available.
CC -1- SIMILARITY: BELONGS TO THE UPK FAMILY.
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C -----
C EMBL: AE001754; AAD35974.1;
C PIR: F72321; F72321.
C TIGR; TW0893;
C HAMAP; MF_01006; -; 1.
C InterPro; IPR003824; BACA.
C Pfam; PF02673; BACA; 1.
C Transferrase; Kinase; Antibiotic resistance; Transmembrane;
K Complete proteome.
FT TRANSMEM 36 55
FT TRANSMEM 67 84
FT TRANSMEM 99 118
FT TRANSMEM 125 147
FT TRANSMEM 167 186
FT TRANSMEM 191 209
FT TRANSMEM 219 236
FT SEQUENCE 237 AA; 26036 MW; 759239335C5FE10F CRC64;

Query Match 4.9%; Score 6; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LDALLV 30
Db 129 LDALLV 134

RESULT 72
PSB6 MOUSE
ID PSB6 MOUSE STANDARD; PRT; 238 AA.
AC Q60692; Q60693;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Proteasome subunit beta type 6 precursor (EC 3.4.25.1) (Proteasome
delta chain) (Macropain delta chain) (Multicatalytic endopeptidase
complex delta chain) (Proteasome subunit Y).
```

N PSMB6 OR LMP19.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
[1]
N SEQUENCE FROM N.A.
P STRAIN=DBA/2J; TISSUE=Liver;
C MEDLINE=95317820; PubMed=7797265;
X Woodward E.C., Monaco J.J.,
T "Characterization and mapping of the gene encoding mouse proteasome
L subunit DELTA (Imp19).";
L Immunogenetics 42:28-34 (1995).
C -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
C WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG,
C PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR
C SLIGHTLY BASIC pH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC
C ACTIVITY. MAY CATALYZE BASAL PROCESSING OF INTRACELLULAR ANTIGENS.
C -1- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
C specificity.
C -1- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal
C proteolytic pathway.
C -1- SUBUNIT: The proteasome is composed of at least 15 non identical
C subunits which form a highly ordered ring-shaped structure. This
C subunit can be displaced by the equivalent immune-specific subunit
C PSMB9.
C -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
C -1- SIMILARITY: Belongs to peptidase family T1B.
C
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C
C EMBL: U13393; AAA75375.1; ALT INIT.
C R EMBL: U13394; AAA75376.1; ALT_INIT.
C R HSP; P38624; IRYP.
C R MEROPS; T01.010; -.
C R MGD; MGI:104880; PsmB6.
C R InterPro: IPR000243; Proteasome_B.
C R InterPro: IPR001353; Proteasome.
C R Pfam: PF00227; Proteasome_1.
C R PRINTS; PR00141; PROTEASOME.
C R PROSITE; PS00854; PROTEASOME_B; 1.
C W Proteasome; Hydrolase; Protease; Zymogen.
C T PROPEP 1 33 BY SIMILARITY.
C T CHAIN 34 238 A -> T.
C T VARIANT 38 38 A -> T.
C T VARIANT 89 89 A -> T.
C T SEQUENCE 238 AA; 25425 MW; 7AEFC23BEE4145A6 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y' 60 RAGSAP 65

Db 9 RAGSAP 14

RESULT 73

HIS4 BRUME ID HIS4 BRUME STANDARD; PRT; 243 AA.

AC Q8VE36; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)

DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide

DE isomerase).
GN HIS4 OR EMBI2042.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
CX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RA MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elser P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
CC phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-
CC [(5-phospho-1-deoxyribulose-1-ylamino)methylideneamino]-1-(5-
CC phosphoribosyl)imidazole-4-carboxamide.
CC -1- PATHWAY: Histidine biosynthesis; fourth step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HIS4 / HISF FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
C EMBL: AB009637; AAL53223.1; -.
C R HAMAP; MF_01014; -.
C R InterPro: IPR003009; FMN enzyme.
C R InterPro: IPR006063; His4.
C R InterPro: IPR006062; His biosynth.
C R Pfam: PF00977; His biosynth; 1.
C R TIGRFAMs; TIGR00007; TIGR00007; 1.
C R isomerase; Histidine biosynthesis; Complete proteome.
C SQ SEQUENCE 243 AA; 25589 MW; 1B264AC48A4D199A CRC64;

Query Match 4.9%; Score 6; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 FPGQVA 36

Db 120 FPGQVA 125

RESULT 74

HIS4 BRUSU ID HIS4 BRUSU STANDARD; PRT; 243 AA.

AC Q8FY08; 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)

DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide

DE isomerase).
GN HIS4 OR BR2084.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
CX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;

```

IX MEDLINE=22247741; PubMed=12711122;
IA Paulsen I.T., Seshadri R., Nelson K.E., Eissen J.A., Heidelberg J.F.,
IA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
IA Daugherty S.C., Deboy R.T., Durkin A.S., Kolony J.F., Madupu R.,
IA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
IA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
IA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
IA "The Brucella suis genome reveals fundamental similarities between
IA animal and plant pathogens and symbionts."
IA Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
IX -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
IX phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-
IX [(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-
IX phosphoribosyl)imidazole-4-carboxamide.
IX -1- PATHWAY: Histidine biosynthesis; fourth step.
IX -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
IX -1- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
IX
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IX or send an email to license@isb-sib.ch).
IX
IX -----
IX EMBL; AE014495; AAK30974.1; -.
IX TIGR; BR2084; -.
IX HAVAP; MF_01014; -.
IX InterPro; IPR003009; FMN enzyme.
IX InterPro; IPR006063; His4.
IX InterPro; IPR006062; His biosynth.
IX Pfam; PF00977; His biosynth; 1.
IX TIGRFAMs; TIGR00007; TIGR00007; 1.
IX Isomerase; Histidine biosynthesis; Complete proteome.
IX SEQUENCE 243 AA; 25601 MW; 2C34672A986CC478 CRC64;
IX
IX Query Match 4.9%; Score 6; DB 1; Length 243;
IX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
IX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
IX
IX QY 31 PFGQVA 36
IX Db 120 PFGQVA 125
IX
IX RESULT 75
IX HIS4_AGR75 STANDARD; PRT; 247 AA.
IX
IX AC P58790;
IX DT 28-FEB-2003 (Rel. 41, Created)
IX DT 28-FEB-2003 (Rel. 41, Last sequence update)
IX DT 28-FEB-2003 (Rel. 41, Last annotation update)
IX DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]
IX imidazole-4-carboxamide isomerase (EC 5.3.1.16)
IX DE (Phosphoribosylformimino-5-aminomidazole carboxamide ribotide
IX isomerase).
IX GN HISA OR ATU0040 OR AGR_C63.
IX OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
IX OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
IX OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
IX NCBI_TaxID=176299;
IX [1]
IX
IX SEQUENCE FROM N.A.
IX MEDLINE=21608550; PubMed=11743193;
IX RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
IX RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
IX RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,
IX RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
IX RA Kutayavin T., Levy R., Li M.J., McLlland E., Palmieri A.,
IX Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
IX Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
IX Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

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RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RA "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
CC phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-
CC [(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-
CC phosphoribosyl)imidazole-4-carboxamide.
CC -1- PATHWAY: Histidine biosynthesis; fourth step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
CC
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CC
CC -----
CC EMBL; AE008978; AAL41071.1; -.
CC EMBL; AE007946; AAK85864.1; -.
CC PIR; A12581; A12581.
CC PIR; G97363; G97363.
CC
CC HAVAP; MF_01014; -.
CC InterPro; IPR003009; FMN enzyme.
CC InterPro; IPR006063; His4.
CC InterPro; IPR006062; His biosynth.
CC Pfam; PF00977; His biosynth; 1.
CC TIGRFAMs; TIGR00007; TIGR00007; 1.
CC Isomerase; Histidine biosynthesis; Complete proteome.
CC SEQUENCE 247 AA; 26027 MW; 9DA6142FEC740104 CRC64;
CC
CC Query Match 4.9%; Score 6; DB 1; Length 247;
CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 31 PFGQVA 36
CC Db 120 PFGQVA 125
CC

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Search completed: February 9, 2004, 12:58:00
Job time : 30 secs

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M protein - protein search, using sw model

un on: February 9, 2004, 12:49:57 ; Search time 52 Seconds
(without alignments)
610.394 Million cell updates/sec

file: US-09-981-876-200

effect score: 123

sequence: 1 MACRLSFLMGLTFLSVSQT.....PVOPEDDADYCVGVGFSP 123

coring table: OLIGO

Gapop 60.0 , Gapext 60.0

searched: 830525 seqs, 258052604 residues

ord size : 0

total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mhc.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rendent.*

12: sp_virus.*

13: sp_vertibrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	8.9	123	11	O61243 mus musculus
2	8	6.5	104	17	Q97W39 sulfolobus
3	8	6.5	195	4	Q8WV17 homo sapien
4	8	6.5	266	4	Q9H611 homo sapien
5	8	6.5	272	11	Q8B172 mus musculus
6	8	6.5	491	5	Q20058 caenorhabdi
7	8	6.5	650	11	Q8B123 mus musculus
8	7	5.7	93	2	Q9X7B6 mycobacteri
9	7	5.7	109	6	Q9N0W5 cryptocolag
10	7	5.7	112	8	Q9XNK0 mytilus sp.
11	7	5.7	135	4	Q9H524 hmo sapien
12	7	5.7	145	17	Q9HN94 halobacteri
13	7	5.7	150	16	Q8FS88 corynebacte
14	7	5.7	243	16	Q93J21 streptomyc
15	7	5.7	252	5	P90688 branchisto
16	7	5.7	252	16	Q8BHP0 xanthomonas

17	7	5.7	256	16	O8DS61	Q8ds61 streptococ
18	7	5.7	258	16	Q8YPV1	Q8ypv1 anabaena sp
19	7	5.7	265	16	Q9VV6	Q9vv6 staphylococ
20	7	5.7	265	16	Q8NXX3	Q8nx3 staphylococ
21	7	5.7	270	2	Q3X5Q2	Q3x5q2 streptomyc
22	7	5.7	272	16	Q9RUS9	Q9rus9 deinococcus
23	7	5.7	289	16	Q8P5T9	Q8p5t9 xanthomonas
24	7	5.7	298	11	Q8K2T7	Q8k2t7 mus musculu
25	7	5.7	307	16	Q8E6E3	Q8e6e3 streptococ
26	7	5.7	307	16	Q8E0S8	Q8e0s8 streptococ
27	7	5.7	313	16	Q8FSW1	Q8fsw1 corynebacte
28	7	5.7	317	16	Q8NLS9	Q8nls9 corynebacte
29	7	5.7	321	16	Q98LJ3	Q98lj3 rhizobium l
30	7	5.7	335	11	Q8BZ35	Q8bz35 mus musculu
31	7	5.7	357	16	Q8PMY5	Q8pm5 xanthomonas
32	7	5.7	371	16	Q9CEM2	Q9cem2 lactococcus
33	7	5.7	375	16	Q8UHK2	Q8uhk2 agrobacteri
34	7	5.7	401	16	Q8X7D8	Q8x7d8 escherichia
35	7	5.7	401	16	Q8FHT5	Q8fht5 escherichia
36	7	5.7	404	2	Q8RSK7	Q8rsk7 uncultured
37	7	5.7	407	11	Q8BPZ8	Q8bpz8 mus musculu
38	7	5.7	415	16	Q8PLC9	Q8plc9 xanthomonas
39	7	5.7	456	2	Q9R6T0	Q9r6t0 synechococ
40	7	5.7	457	16	Q8XSS9	Q8xss9 raietonia s
41	7	5.7	462	16	Q9RYH5	Q9ryh5 deinococcus
42	7	5.7	464	16	Q8ZFP3	Q8zfz3 versinia pe
43	7	5.7	468	5	Q8G5Z8	Q8g5z8 drosophila
44	7	5.7	468	5	Q9V175	Q9v175 drosophila
45	7	5.7	468	5	Q8MQM1	Q8mqm1 drosophila
46	7	5.7	484	17	Q9HQW0	Q9hqw0 halobacteri
47	7	5.7	518	16	Q8ZP05	Q8zp05 salmonella
48	7	5.7	519	16	Q8Z674	Q8z674 salmonella
49	7	5.7	526	16	Q8ZNO8	Q8zng8 salmonella
50	7	5.7	526	16	Q8ZSG3	Q8zsg3 salmonella
51	7	5.7	526	16	Q8XQP9	Q8xqp9 raietonia s
52	7	5.7	528	16	Q8ZFZ6	Q8zfz6 versinia pe
53	7	5.7	537	16	Q8D075	Q8d075 versinia pe
54	7	5.7	549	16	Q8X7L8	Q8x7l8 escherichia
55	7	5.7	549	16	Q8FG11	Q8fg11 escherichia
56	7	5.7	553	5	Q9U203	Q9u203 caenorhabdi
57	7	5.7	558	10	Q9SNV7	Q9snv7 chlamydomon
58	7	5.7	614	5	P91720	P91720 drosophila
59	7	5.7	659	5	Q9U202	Q9u202 caenorhabdi
60	7	5.7	689	5	Q8WPL5	Q8wpl5 oikopleura
61	7	5.7	701	16	Q8G4I2	Q8g4i2 bifidobacte
62	7	5.7	828	12	Q993H5	Q993h5 callitrichi
63	7	5.7	1443	5	Q8WTB2	Q8wtb2 drosophila
64	7	5.7	1512	2	Q93HF2	Q93hf2 streptomyc
65	7	5.7	1765	5	Q9VS30	Q9vs30 drosophila
66	7	5.7	1770	5	Q9VS29	Q9vs29 drosophila
67	7	5.7	2852	2	Q8A21	Q8a21 vibrio mari
68	7	5.7	4051	5	Q8Z04	Q8z24 plasmodium
69	6	4.9	21	4	Q9NRI7	Q9nri7 homo sapien
70	6	4.9	43	6	Q28453	Q28453 leontosteli
71	6	4.9	56	5	Q9U447	Q9u447 dictyosteli
72	6	4.9	56	12	Q96829	Q96829 hepatitis a
73	6	4.9	61	17	Q8TJT4	Q8tjt4 methanosarc
74	6	4.9	61	17	Q8P297	Q8p297 methanosarc
75	6	4.9	64	10	Q8LRE7	Q8lre7 oryza sativ
76	6	4.9	72	10	Q5FR81	Q5fr81 pisum sativ
77	6	4.9	76	2	Q9J9Z6	Q9j9z6 anabaena sp
78	6	4.9	80	4	Q8N4H1	Q8n4h1 homo sapien
79	6	4.9	80	16	Q9RZA2	Q9rza2 deinococcus
80	6	4.9	81	16	Q9I322	Q9i322 pseudomonas
81	6	4.9	87	10	Q9ZRM9	Q9zrm9 onobrychis
82	6	4.9	88	16	Q94E0	Q94e0 rhizobium l
83	6	4.9	95	16	Q9ZC4	Q9z2c4 rhizobium m
84	6	4.9	99	2	Q9F8G2	Q9f8g2 carboxyloth
85	6	4.9	99	16	Q9SLW3	Q9slw3 streptomyc
86	6	4.9	101	4	Q8LZD8	Q8lzd8 homo sapien
87	6	4.9	103	16	O06257	O06257 mycobacteri
88	6	4.9	105	2	Q9AMS9	Q9ams9 bradyrhizob
89	6	4.9	107	4	Q9NSD6	Q9nsd6 homo sapien

90 6 4.9 107 10 Q24128 nicotiana t
91 6 4.9 109 4 Q9UL86
92 6 4.9 109 4 Q9UL78
93 6 4.9 110 4 Q8T863
94 6 4.9 112 8 Q9T8G6
95 6 4.9 112 8 Q9T8G9
96 6 4.9 114 9 Q38281
97 6 4.9 116 10 Q8H2X6
98 6 4.9 117 2 Q9XDGI
99 6 4.9 117 8 Q79922
100 6 4.9 117 16 Q9PB24

ALIGNMENTS

3 RESULT 1
ID Q61243 PRELIMINARY; PRT; 123 AA.
AC Q61243;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE SHS20 protein precursor (Pre-B lymphocyte gene 3).
EN VPBE3.
DS Mus musculus (Mouse).
DC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DX NCBI_TaxID=10090;
XN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=93259124; PubMed=8491176;
RA Shirasawa T., Ohnishi K., Hagiwara S., Shigemoto K., Takebe Y.,
RA Rajewsky K., Takemori T.,
RT "A novel gene product associated with mu chains in immature B cells."
RL EMBL J. 12:1827-1834(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoerbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; D13208; BAA02495.1; -;
DR EMBL; AK008754; BAE25899.1; -;
DR HSSP; P01709; ZMCG.
DR MGD; MGI:98938; Vpreb3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1. SHS20 PROTEIN.
FT CHAIN 20 123
SQ SEQUENCE 123 AA; 13400 MW; 2A1AD371DICE98F CRC64;

Query Match 8.9%; Score 11; DB 11; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 RPADIPDRFSA 89
Db |||||
79 RPADIPDRFSA 89
RESULT 2
Q97W39 PRELIMINARY; PRT; 104 AA.
ID Q97W39;
AC Q97W39;
DT 01-OCT-2001 (TEMBLrel. 18, Created)
DT 01-OCT-2001 (TEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TEMBLrel. 18, Last annotation update)
DE Hypothetical protein SSO2405.
GN SSO2405.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
XN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweyaz M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006841; AAK42551.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 104 AA; 12215 MW; 18CB0F9C56FBI391 CRC64;

Query Match 6.5%; Score 8; DB 17; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQLDALIV 30
Db |||||
70 AQLDALIV 77
RESULT 3
Q8WV17 PRELIMINARY; PRT; 195 AA.
ID Q8WV17;
AC Q8WV17;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Similar to hypothetical protein FLJ22692.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
XN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Placenta;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018978; AAH18978.1; -;
KW Hypothetical protein.
SQ SEQUENCE 195 AA; 21312 MW; C1971DEEOBA8218 CRC64;

Query Match 6.5%; Score 8; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Q20058
ID Q20058 PRELIMINARY; PRT; 491 AA.
AC Q20058;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE F35G12.12 protein.
GN F35G12.12
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Chui C.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. PubMed=9851916;
RX MEDLINE=99069613;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; 246242; CRA86334.2; -.
DR WormPep; F35G12.12; CE31499.
SQ SEQUENCE 491 AA; 55833 MW; 89F86FD9C6E56883E CRC64;

Query Match 6.5%; Score 8; DB 5; Length 491;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQLDAL 28
Db 208 VLAQLDAL 215

RESULT 7
Q8BIZ3 PRELIMINARY; PRT; 650 AA.
AC Q8BIZ3;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE DNA helicase homolog homolog.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RA MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK049353; BAC33702.1; -.
SQ SEQUENCE 650 AA; 70941 MW; 0330ABA54006DDE4 CRC64;

Query Match 6.5%; Score 8; DB 11; Length 650;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108
Db 162 TISPVQPE 169

RESULT 8
Q9X7B6 PRELIMINARY; PRT; 93 AA.
ID Q9X7B6
AC Q9X7B6;
```

YT 01-NOV-1999 (TrEMBLrel. 12, Created)
YT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
YT 01-DEC-2001 (TrEMBLrel. 12, Last annotation update)
ZE Hypothetical 10.5 kDa protein.
ZN MLCB1610.18.
XS Mycobacterium leprae.
XC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
XC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
XN NCBI_TaxID=1769;
IP SEQUENCE FROM N.A.
IP Seeger K.J., Harris D.;
IL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
XN NCBI_TaxID=1769;
IP SEQUENCE FROM N.A.
XA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
XL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
XN NCBI_TaxID=1769;
XP SEQUENCE FROM N.A.
XX MEDLINE=93188700; PubMed=8446027;
XA Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
RT "Use of an ordered cosmid library to deduce the genomic organization
RT of Mycobacterium leprae";
XL Mol. Microbiol. 7:197-206(1993).
XN EMBL; AL049913; CAB43164.1; --
KW Hypothetical protein.
SQ SEQUENCE 93 AA; 10527 MW; E530B3B666CA52FB CRC64;
Query Match 5.7%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 GSAPRYL 68
DB 23 GSAPRYL 29
RESULT 9
Q9N0W5 PRELIMINARY; PRT; 109 AA.
AC Q9N0W5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-human A33 light chain variable region (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20250927; PubMed=10788485;
RA Rader C., Ritter G., Nathan S., Elia M., Gout I., Jungbluth A.A.,
RA Cohen L.S., Welt S., Old L.J., Barbas C.F. III.;
RT "The rabbit antibody repertoire as a novel source for the generation
RT of therapeutic human antibodies";
RL J. Biol. Chem. 275:13668-13676(2000).
DR EMBL; AF245502; AAF68449.1; --
DR HSSP; P80362; 1WTI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11323 MW; BD8B396EE75F94FB CRC64;
Query Match 5.7%; Score 7; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSWTQQ 59
DB 32 GVSWTQQ 38
RESULT 10
Q9XNK0 PRELIMINARY; PRT; 112 AA.
AC Q9XNK0
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cytochrome c oxidase subunit III (EC 1.9.3.1) (Cytochrome c oxidase
DE polypeptide III) (Fragment).
GN COIII.
OS Mytilus sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=61855;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim I., Min B.-Y., Yoon M.-H., Yoo M.-S., Kim D.-H.;
RT "Unusual mitochondrial DNA polymorphism of the blue mussel (Mytilus
RT edulis) species complex on the southern coast of Korea";
RL Korean J. Biol. Sci. 3:79-87(1999).
CC -1- FUNCTION: SUBUNITS I, II AND III FORM THE FUNCTIONAL CORE OF THE
CC ENZYME COMPLEX (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
CC C + 2 H(2)O.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
CC EMBL; AF127466; AAD43264.1; --
DR InterPro; IPR000298; CytC_oxdse_III.
DR Pfam; PF00510; COX3; 1.
DR ProDom; PD000382; CytC_oxdse_III; 1.
DR PROSITE; PS50253; COX3; 1.
KW Oxidoreductase; Transmembrane; Mitochondrion.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12930 MW; 143696990AC473E2 CRC64;
Query Match 5.7%; Score 7; DB 8; Length 112;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 SFLLMGT 13
DB 9 SFLLMGT 15
RESULT 11
Q9H5Z4 PRELIMINARY; PRT; 135 AA.
AC Q9H5Z4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ22755.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ileal mucosa;
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Serba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026408; BAB15473.1; --

R HSP; P01607; 1REI.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; ig; 1.
R SMART; SM00406; IGv; 1.
W Hypothetical protein.
Q SEQUENCE 135 AA; 14780 MW; 652492DED930P401 CRC64;
Query Match 5.7%; Score 7; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 65 PRVLYX 71
b 24 PRVLYX 30
RESULT 12
9HN94 PRELIMINARY; PRT; 145 AA.
C Q9HN94;
D 01-MAR-2001 (T-EMBLrel. 16, Created)
T 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
E Cytochrome c oxidase subunit II.
T Cytochrome c oxidase subunit II.
N COX2 OR VNG2195G.
S Halobacterium sp. (strain NRC-1).
C Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
C Halobacteriaceae; Halobacterium.
X NCBI_TaxID=64091;
N [1]
F SEQUENCE FROM N.A.
X MEDLINE=20504483; PubMed=11016950;
A NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shrogha J.,
A Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
A Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A Isenbarger T.A., Peck R.F., Pohlischroder M., Spudich J.L., Jung K.-H.,
A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
T "Genome sequence of Halobacterium species NRC-1.";
L Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
C -1- COPACTOR: COPPER A AND HEME GROUP (BY SIMILARITY)
C -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
C -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.
R EMBL; AE005106; AAG20327.1; -.
R HSP; P98052; 1EHK.
R InterPro; IPR001505; Copper_CuA.
R InterPro; IPR002429; Cyt_c_ox_2.
R Pfam; PF00116; COX2; 1.
R ProDom; PD000131; Copper_CuA; 1.
R PROSITE; PS00078; COX2; 1.
W Copper; Oxidoreductase; Complete proteome.
Q SEQUENCE 145 AA; 15591 MW; 3D67301DB92E887C CRC64;
Query Match 5.7%; Score 7; DB 17; Length 145;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 32 PGQVAQL 38
b 86 PGQVAQL 92
RESULT 13
9FSS8 PRELIMINARY; PRT; 150 AA.
C Q9FSS8;
D 01-MAR-2003 (T-EMBLrel. 23, Created)
T 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
E Hypothetical protein.
N NCBI_TaxID=64091;
F SEQUENCE FROM N.A.
X MEDLINE=20504483; PubMed=11016950;
A NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shrogha J.,
A Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
A Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A Isenbarger T.A., Peck R.F., Pohlischroder M., Spudich J.L., Jung K.-H.,
A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
T "Genome sequence of Halobacterium species NRC-1.";
L Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
C -1- COPACTOR: COPPER A AND HEME GROUP (BY SIMILARITY)
C -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
C -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.
R EMBL; AE005106; AAG20327.1; -.
R HSP; P98052; 1EHK.
R InterPro; IPR001505; Copper_CuA.
R InterPro; IPR002429; Cyt_c_ox_2.
R Pfam; PF00116; COX2; 1.
R ProDom; PD000131; Copper_CuA; 1.
R PROSITE; PS00078; COX2; 1.
W Copper; Oxidoreductase; Complete proteome.
Q SEQUENCE 145 AA; 15591 MW; 3D67301DB92E887C CRC64;

GN CE0304.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005215; BAC17114.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 150 AA; 16043 MW; 800D03C94769F9FE CRC64;
Query Match 5.7%; Score 7; DB 16; Length 150;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 RAGSAPR 66
Db 82 RAGSAPR 88
RESULT 14
93J21 PRELIMINARY; PRT; 243 AA.
ID Q93J21
AC Q93J21;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DE Putative GntR-family transcriptional regulator.
OS SCO3986 OR SCBAC25E3.23.
GN Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Collins M., Harris D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RC MEDLINE=97000351; PubMed=8843436;
RX Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RP Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";

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RL Nature 417:141-147(2002).
CC -!- SIMILARITY: BELONGS TO THE GNTN FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -!- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AL939118; CAC44710.1; -.
DR InterPro; IPR000524; HTH_GntR.
DR Pfam; PF00392; gntR; 1.
DR PRINTS; PR00035; HTHGNTN.
DR SMART; SM00345; HTH GNTN; 1.
DR PROSITE; PS00043; HTH GNTN FAMILY; 1.
KW DNA-binding; Transcription-regulation; Complete proteome.
SQ SEQUENCE 243 AA; 26537 MW; 731CDBE7A9CF8ED3 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 243;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALLVFP 33
DB 217 ALLVFP 223

RESULT 15
P90688
ID P90688 PRELIMINARY; PRT; 252 AA.
AC P90688;
JT 01-MAY-1997 (TrEMBLrel. 03, Created)
JT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
JT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Engrailed protein.
EN AMPHEN.
CS Branchiostoma floridae (Florida lancelet) (Amphioxus).
CC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
CC Branchiostoma.
CX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97307778; PubMed=9165120;
RA Holland L.Z., Kene M., Williams N.A., Holland N.D.;
RT "Sequence and metryonic expression of the amphioxus engrailed gene
RT (Amphixn): the metameric pattern of transcription resembles that of
RT its segment-polarity homolog in Drosophila."
RL Development 124:1723-1732(1997).
CC -!- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U82487; AAB40144.1; -.
DR HSP; P02836; 3HDD.
DR InterPro; IPR000747; Engrailed.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepreser.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00026; ENGRAILED.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRINTS; PR00010; Homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00033; ENGRAILED; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 252 AA; 27817 MW; D3A52A9DB44BA39F CRC64;

Query Match 5.7%; Score 7; DB 5; Length 252;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SPVQPED 109
DB 21 SPVQPED 27

RESULT 16
Q9PFP0

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ID Q9PFP0 PRELIMINARY; PRT; 252 AA.
AC Q9PFP0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Trehalose-6-phosphate phosphatase.
GN OSTB OR XAC3209.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
CX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.F., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Spindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011966; AAM38053.1; -.
DR InterPro; IPR006379; HAD_SF_IIB.
DR InterPro; IPR003337; Trehalose_PPase.
DR Pfam; PF02358; Trehalose_PPase_1.
DR TIGRFAMs; TIGR01484; HAD-SF-IIB; 1.
DR TIGRFAMs; TIGR00685; T6P; 1.
KW Complete proteome.
SQ SEQUENCE 252 AA; 27029 MW; C50CF23E1CA2C1D9 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 252;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LAQLDAL 28
DB 67 LAQLDAL 73

RESULT 17
Q9DS61
ID Q9DS61 PRELIMINARY; PRT; 256 AA.
AC Q9DS61;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative pyrroline carboxylate reductase (EC 1.5.1.2).
GN PROC OR SMU.1974.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=UAI59 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savić G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen."

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L Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
R EMBL: A3015020; AAN59579.1; -.
W Oxidoreductase; Complete proteome.
Q SEQUENCE 256 AA; 27101 MW; 0BAA131398EB60AF CRC64;

Query Match 5.7%; Score 7; DB 16; Length 256;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 17 VSQTVLA 23
| | | | |
b 194 VSQTVLA 200

RESULT 18
81PVL PRELIMINARY; PRT; 258 AA.
D Q8YPLV;
C Q8YPLV;
T 01-MAR-2002 (TrEMBLrel. 20, Created)
T 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
T 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E Hypothetical protein A114089.
N ALL4089.
S Anabaena sp. (strain PCC 7120).
C Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
X NCBI_TaxID=103690;
N [1]
P SEQUENCE FROM N.A.
X MEDLINE=21595285; PubMed=11759840;
A Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
A Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
A Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
A Yasuda M., Tabata S.;
T "Complete genomic sequence of the filamentous nitrogen-fixing
T cyanobacterium Anabaena sp. strain PCC 7120.";
L DNA Res. 8:205-213 (2001).
L EMBL: AP003595; BAB75788.1; -.
W Hypothetical protein; Complete proteome.
Q SEQUENCE 258 AA; 29638 MW; 741FBC39089ECA49 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 258;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 19 QTVLAQL 25
| | | | |
b 92 QTVLAQL 98

RESULT 19
J99VV6 PRELIMINARY; PRT; 265 AA.
D Q99VV6;
C Q99VV6;
T 01-JUN-2001 (TrEMBLrel. 17, Created)
T 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
T 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E SA0620 protein (Secretory antigen Ssa homologue).
N SAV0665 OR SA0620.
S Staphylococcus aureus (strain Mu50 / ATCC 700699), and
S Staphylococcus aureus (strain N315).
C Bacteria; Firmicutes; Bacillales; Staphylococcus.
X NCBI_TaxID=158878, 158879;
N [1]
P SEQUENCE FROM N.A.
C SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
X MEDLINE=21311952; PubMed=11418146;
A Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
A Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
A Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
A Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
A Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
A Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus.";
RL Lancet 357:1225-1240 (2001).
DR EMBL: AP003360; BAB56827.1; -.
DR EMBL: AP003131; BAB41853.1; -.
DR InterPro: IPR002482; LysM.
DR Pfam: PF01476; LysM; 2.
DR SMART: SM00257; LysM; 2.
KW Complete proteome.
SQ SEQUENCE 265 AA; 28187 MW; 16A8159D0F3C0285 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LVFPGQV 35
| | | | |
Db 61 LVFPGQV 67

RESULT 20
Q8NKR3 PRELIMINARY; PRT; 265 AA.
ID Q8NKR3
AC Q8NKR3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MW0627 protein.
GN MW0627.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Tamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
DR EMBL: AP004824; BAB94492.1; -.
DR InterPro: IPR002482; LysM.
DR Pfam: PF01476; LysM; 2.
KW Complete proteome.
SQ SEQUENCE 265 AA; 28173 MW; 0958118E183F1696 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LVFPGQV 35
| | | | |
Db 61 LVFPGQV 67

RESULT 21
Q9X5Q2 PRELIMINARY; PRT; 270 AA.
ID Q9X5Q2
AC Q9X5Q2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Milt.
GN Milt.
OS Streptomyces lavendulae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1914;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 2564;

```

XX MEDLINE=99201491; PubMed=10099135;
Xt Mao Y., Varoglu M., Sherman D.H.;
Xt "Molecular characterization and analysis of the biosynthetic gene
Xt cluster for the antitumor antibiotic mitomycin C from Streptomyces
Xt lavendulae NRRL 2564."
Xl Chem. Biol. 6:251-263(1999).
Xl EMBL: AF127374; AAD28452.1; -.
Xl InterPro: IPR000205; NAD binding.
Xl InterPro: IPR006155; Shikimate DH.
Xl InterPro: IPR000594; Thif_ domain.
Xl Pfam: PF01488; Shikimate DH; 1.
Xl SEQUENCE 270 AA; 28130 MW; F6537EB0949C77FE CRC64;

Query Match 5.7%; Score 7; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 23 AQLDALL 29
2b 168 AQLDALL 174

RESULT 22
X9RUS9 ID Q9RUS9 PRELIMINARY; PRT; 272 AA.
Xc STRAIN=RL;
Xx MEDLINE=20036896; PubMed=10567286;
Xx White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Xx Dodson R.J., Hart D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
Xx Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Xx Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Xx Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Xx Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Xx Fraser C.N.;
Xt "Genome sequence of the radioresistant bacterium Deinococcus
Xt radiodurans R1."
Xl Science 286:1571-1577(1999).
Xl EMBL: AE001977; AAF10873.1; -.
Xl TIGR: DR1303; -.
Xl InterPro: IPR000515; BPD_transp.
Xl Pfam: PF00528; BPD_transp; 1.
Xl PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; 1.
Xl Complete proteome.
Xl SEQUENCE 272 AA; 30264 MW; 0DA0CF07D6BA6A3F CRC64;

Query Match 5.7%; Score 7; DB 16; Length 272;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 6 LSFLIM 12
2b 244 LSFLIM 250

RESULT 23
X9P5T9 ID Q9P5T9 PRELIMINARY; PRT; 289 AA.
Xc STRAIN=RL;
Xx MEDLINE=20036896; PubMed=10567286;
Xx White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Xx Dodson R.J., Hart D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
Xx Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Xx Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Xx Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Xx Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Xx Fraser C.N.;
Xt "Genome sequence of the radioresistant bacterium Deinococcus
Xt radiodurans R1."
Xl Science 286:1571-1577(1999).
Xl EMBL: AE001977; AAF10873.1; -.
Xl TIGR: DR1303; -.
Xl InterPro: IPR000515; BPD_transp.
Xl Pfam: PF00528; BPD_transp; 1.
Xl PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; 1.
Xl Complete proteome.
Xl SEQUENCE 272 AA; 30264 MW; 0DA0CF07D6BA6A3F CRC64;

Query Match 5.7%; Score 7; DB 16; Length 272;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 6 LSFLIM 12
2b 244 LSFLIM 250

RESULT 23
X9P5T9 ID Q9P5T9 PRELIMINARY; PRT; 289 AA.
Xc STRAIN=RL;
Xx MEDLINE=20036896; PubMed=10567286;
Xx White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Xx Dodson R.J., Hart D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
Xx Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Xx Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Xx Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Xx Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Xx Fraser C.N.;
Xt "Genome sequence of the radioresistant bacterium Deinococcus
Xt radiodurans R1."
Xl Science 286:1571-1577(1999).
Xl EMBL: AE001977; AAF10873.1; -.
Xl TIGR: DR1303; -.
Xl InterPro: IPR000515; BPD_transp.
Xl Pfam: PF00528; BPD_transp; 1.
Xl PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; 1.
Xl Complete proteome.
Xl SEQUENCE 272 AA; 30264 MW; 0DA0CF07D6BA6A3F CRC64;

Query Match 5.7%; Score 7; DB 11; Length 298;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 107 PEDDADY 113
2b 107 PEDDADY 113

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DE Transcriptional regulator.
GN XCC3246.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
RL EMBL: AB012442; AAM42516.1; -.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam: PF00426; HTH_1; 1.
DR Pfam: PF03466; LysR_substrate; 1.
DR PRINTS: PR00039; HTHLYSR.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
KW Complete proteome.
SQ SEQUENCE 289 AA; 31936 MW; 3B0D47F87512F912 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 289;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 LAQLDAL 28
Db 131 LAQLDAL 137

RESULT 24
Q8K2T7 ID Q8K2T7 PRELIMINARY; PRT; 298 AA.
AC Q8K2T7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to hypothetical protein FLJ13614.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC029845; AAB29845.1; -.
KW Hypothetical protein.
SQ SEQUENCE 298 AA; 33669 MW; 34CD1CE3AD80B7FB CRC64;

Query Match 5.7%; Score 7; DB 11; Length 298;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 PEDDADY 113
Db 107 PEDDADY 113

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Db      286 PEDDADY 292

RESULT 25
Q8E6E3
ID Q8E6E3 PRELIMINARY; PRT; 307 AA.
AC Q8E6E3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
EN GBS0629.

OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RC STRAIN=NM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaeser P., Rusnink C., Buchrieser C., Chevalier P., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766846; CAD46273.1; -.
DR SAGaList; gbs0629; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 307 AA; 33928 MW; 5D359E74AFD40C16 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 307;
Best Local Similarity 100.0%; Pred. No. 77; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

2Y 18 SQTVLAQ 24
Db 22 SQTVLAQ 28

RESULT 26
Q8E0S8
ID Q8E0S8 PRELIMINARY; PRT; 307 AA.
AC Q8E0S8
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cell wall surface anchor family protein.
EN SAG0646.

OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547;
RA Tettelin H., Masiognani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy A.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014220; AAM99538.1; -.
DR TIGR; SAG0646; -.
KW Complete proteome.
SQ SEQUENCE 307 AA; 33928 MW; 5D359E74AFD40C16 CRC64;
```

Query Match 5.7%; Score 7; DB 16; Length 307;
Best Local Similarity 100.0%; Pred. No. 77; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 18 SQTVLAQ 24
Db 22 SQTVLAQ 28

RESULT 27

Q8FSW1
ID Q8FSW1 PRELIMINARY; PRT; 313 AA.
AC Q8FSW1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative thioredoxin reductase.
EN CE2933.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005224; BAC19743.1; -.
KW Complete proteome.
SQ SEQUENCE 313 AA; 34025 MW; 602AF9C5A5FC961F CRC64;

Query Match 5.7%; Score 7; DB 16; Length 313;
Best Local Similarity 100.0%; Pred. No. 78; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 62 GSAPRYL 68
Db 116 GSAPRYL 122

RESULT 28

Q8NL59
ID Q8NL59 PRELIMINARY; PRT; 317 AA.
AC Q8NL59
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Thioredoxin reductase (EC 1.6.4.5).
EN CGL3090.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005283; BAC00484.1; -.
DR InterPro; IPR000759; Adrtdx_reductase.
DR InterPro; IPR001327; PAD_pyrd_redox.
DR InterPro; IPR001013; Pyridine_redox.
DR InterPro; IPR003042; Rng_mnoxysgenase.
DR InterPro; IPR005982; Thioredox_reduct.
DR Pfam; PF000070; Pyr_redox; 1.
DR PRINTS; PR00419; ADXRTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00469; PNDRTASEII.

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DR PRINTS; PRO0420; RINGNOXGNASE.
DR TIGRPMG; TIGR01292; TRX reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 317 AA; 34255 MW; DB290007549BB457 CRC64;

Query Match      5.7%; Score 7; DB 16; Length 317;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GSAPRYL 68
DB 120 GSAPRYL 126

RESULT 29
Q98LI3 PRELIMINARY; PRT; 321 AA.
AC Q98LI3;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein mill1010.
GN MLI1010.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RL Mesorhizobium loti."
RL DNA Res 7:331-338(2000).
DR EMBL; AF002996; BAB48480.1; --
DR InterPro; IPR002220; DHDPS.
DR Pfam; PF00701; DHDPS; 1.
DR PRINTS; PRO0146; DHPICNSTHASE.
DR ProDom; PD001859; DHDPS; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 321 AA; 34990 MW; 1FA700B822B8CF95 CRC64;

Query Match      5.7%; Score 7; DB 16; Length 321;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DALLVFP 32
DB 107 DALLVFP 113

RESULT 30
Q8BZ35 PRELIMINARY; PRT; 335 AA.
AC Q8BZ35;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical aminoacyl-transfer RNA synthetases class-II containing
DE protein.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Vagina;

DR PRINTS; PRO0420; RINGNOXGNASE.
DR TIGRPMG; TIGR01292; TRX reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 317 AA; 34255 MW; DB290007549BB457 CRC64;

Query Match      5.7%; Score 7; DB 16; Length 317;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GSAPRYL 68
DB 120 GSAPRYL 126

RESULT 29
Q98LI3 PRELIMINARY; PRT; 321 AA.
AC Q98LI3;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein mill1010.
GN MLI1010.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RL Mesorhizobium loti."
RL DNA Res 7:331-338(2000).
DR EMBL; AF002996; BAB48480.1; --
DR InterPro; IPR002220; DHDPS.
DR Pfam; PF00701; DHDPS; 1.
DR PRINTS; PRO0146; DHPICNSTHASE.
DR ProDom; PD001859; DHDPS; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 321 AA; 34990 MW; 1FA700B822B8CF95 CRC64;

Query Match      5.7%; Score 7; DB 16; Length 321;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DALLVFP 32
DB 107 DALLVFP 113

RESULT 30
Q8BZ35 PRELIMINARY; PRT; 335 AA.
AC Q8BZ35;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical aminoacyl-transfer RNA synthetases class-II containing
DE protein.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Vagina;

RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK036810; BAC29587.1; --
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 36950 MW; 3D4875D4FF548219 CRC64;

Query Match      5.7%; Score 7; DB 11; Length 335;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 OLDALLY 30
DB 305 OLDALLY 311

RESULT 31
Q8PMY5 PRELIMINARY; PRT; 357 AA.
AC Q8PMY5;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE 2-nitropropane dioxygenase.
GN XAC1290.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RC MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formigueri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011759; AAM36161.1; --
DR InterPro; IPR004136; 2nprop dioxygen.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF03060; NPD; 1.
KW Dioxygenase; Complete proteome.
SQ SEQUENCE 357 AA; 36732 MW; 7437EB83901C84C0 CRC64;

Query Match      5.7%; Score 7; DB 16; Length 357;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AOLDALL 29
DB 118 AOLDALL 124

RESULT 32
Q9CEM2 PRELIMINARY; PRT; 371 AA.
ID Q9CEM2

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Q9CEM2; 2001 (TrEMBLrel. 17, Created)
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 Permease.
 N YSIB OR L11815.
 S Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 C Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 X NCBI_TaxID=1360;
 [1]
 P SEQUENCE FROM N.A.
 C STRAIN=IL1403;
 MEDLINE=21235186; PubMed=11337471;
 A Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
 A Weisenbach J., Ehrlich S.D., Sorokin A.,
 T "The complete genome sequence of the lactic acid bacterium Lactococcus
 T lactis ssp. lactis IL1403."
 L Genome Res. 11:731-753(2001).
 R EMBL; AE006411; AAK05913.1; -.
 R InterPro; IPR002549; UPF0118.
 R Pfam; PF01594; UPF0118; 1.
 R Complete proteome.
 R SEQUENCE 371 AA; 41524 MW; 4CF474A1FDA1289A CRC64;

Query Match 5.7%; Score 7; DB 16; Length 371;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 25 LDALLVP 31
 [1]
 b 229 LDALLVP 235

RESULT 33
 8UHK2 PRELIMINARY; PRT; 375 AA.
 C Q8UHK2
 D Q8UHK2; 2002 (TrEMBLrel. 21, Created)
 T 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 E Histidyl-tRNA synthetase.
 N HISS OR ATU0678 OR AGR C 1214.
 S Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 C Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 X Rhizobiaceae; Rhizobium.
 X NCBI_TaxID=176299;
 [1]
 N SEQUENCE FROM N.A.
 X MEDLINE=21608550; PubMed=11743193;
 A Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 A Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 A Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,
 A Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 A Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 A Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 A Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 A Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 A Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 A Nester E.W.;
 T "The genome of the natural genetic engineer Agrobacterium tumefaciens
 T C58."
 T Science 294:2317-2323(2001).
 [2]
 X SEQUENCE FROM N.A.
 X MEDLINE=21608551; PubMed=11743194;
 A Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
 A Qurollo B., Goldman B.S., Cao Y., Askenazi M., Hatching C., Mullin L.,
 A Houmieu K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,
 A Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 A Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 A Cielo C., Slater S.
 T "Genome sequence of the plant pathogen and biotechnology agent
 T Agrobacterium tumefaciens C58."

RL Science 294:2323-2328(2001).
 DR EMBL; AE009036; AAL41694.1; -.
 DR EMBL; AE008002; AAK86487.1; -.
 KW Aminoacyl-tRNA synthetase; Complete proteome.
 SQ SEQUENCE 375 AA; 40755 MW; B1FABE4ECADCE6AD CRC64;

Query Match 5.7%; Score 7; DB 16; Length 375;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQDALL 29
 [1]
 Db 173 AQDALL 179

RESULT 34
 Q8X7D8 PRELIMINARY; PRT; 401 AA.
 AC Q8X7D8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Putative oxidoreductase.
 GN YCIW OR Z2513 OR ECS1860.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RC MEDLINE=21074935; PubMed=11208551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Gotsfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
 RT Nature 409:529-533(2001).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=O157:H7 / RIMD 0509952;
 RC MEDLINE=21156231; PubMed=11258796;
 RX Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12."
 RL DNA Res. 8:11-22(2001).
 DR EMBL; AE005378; AAG56525.1; -.
 DR EMBL; AP002556; BAB3283.1; -.
 KW Complete proteome.
 SQ SEQUENCE 401 AA; 45189 MW; DA83621180F25577 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 401;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 PDRFSA 90
 [1]
 Db 356 PDRFSA 362

RESULT 35
 Q8FHT5 PRELIMINARY; PRT; 401 AA.
 ID Q8FHT5
 AC Q8FHT5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein yciW.

```
3N YCIW OR C1758.
3S Escherichia coli O6.
3C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
3C Enterobacteriaceae; Escherichia.
3X NCBI_taxID=217992;
3N [1]_taxID=217992;
3P SEQUENCE FROM N.A.
3C STRAIN=C6:HI / CFT073 / ATCC 700928;
3X MEDLINE=2238234; PubMed=12471157;
3A Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
3A Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
3A Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
3A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
3R "Extensive mosaic structure revealed by the complete genome sequence
3T of uropathogenic Escherichia coli."
3T Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
3L EMBL; AE016760; AAN80224.1; -
3W Hypothetical protein; Complete proteome.
3Q SEQUENCE 401 AA; 45077 MW; 9F36B59BEC6FFA70 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 97; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 84 PDRFSAA 90
DB 356 PDRFSAA 362
[1]_taxID=77133;

RESULT 36
Q8RSK7 PRELIMINARY; PRT; 404 AA.
AC Q8RSK7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 42.6 kDa protein.
OS uncultured bacterium.
OG Plasmid pB4.
OC Bacteria; environmental samples.
OX NCBI_taxID=77133;
RN [1]_taxID=77133;
RP SEQUENCE FROM N.A.
RA Tauch A.;
RT "The IncP beta plasmid pB4 encodes a tripartite antibiotic efflux
RT system of the RND-MFP-DEF type conferring erythromycin and
RT roxithromycin resistance in Pseudomonas sp. B13."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A7431260; CAD24357.1; -
DR InterPro; IPR003439; ABC transporter.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 404 AA; 42586 MW; ECAE469A421602A6 CRC64;

Query Match 5.7%; Score 7; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 97; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 22 LAQLDAL 28
DB 172 LAQLDAL 178
[1]_taxID=77133;

RESULT 37
Q8BPZ8 PRELIMINARY; PRT; 407 AA.
AC Q8BPZ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

50 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
50 NCBI_taxID=10090;
50 [1]_taxID=10090;
50 SEQUENCE FROM N.A.
50 MEDLINE=C57BL/6J; TISSUE=Eye;
50 MEDLINE=22354683; PubMed=12466851;
50 The FANTOM Consortium.
50 the RIKEN Genome Exploration Research Group Phase I & II Team;
50 "Analysis of the mouse transcriptome based on functional annotation of
50 60,770 full-length cDNAs."
50 Nature 420:563-573(2002).
50 EMBL; AK051816; BAC34780.1; -
50 Hypothetical protein.
50 SEQUENCE 407 AA; 46039 MW; FB8B05A197A2BC64 CRC64;

Query Match 5.7%; Score 7; DB 11; Length 407;
Best Local Similarity 100.0%; Pred. No. 98; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 107 PEDDADY 113
DB 395 PEDDADY 401
[1]_taxID=92829;

RESULT 38
Q8PLC9 PRELIMINARY; PRT; 415 AA.
AC Q8PLC9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Inner membrane protein.
GN XAC1873.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_taxID=92829;
RN [1]_taxID=92829;
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Ciarrelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Lenos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos A.M.B.N., Martinez-Rossi N.M.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meidanis J., Menck C.F.M., Oliveira M.C., Oliveira V.R.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Silva C., de Souza R.F.,
RA Pereira H.A.F., Rossi A., Sena J.A.D., Silva C., Teixeira B.C., Tezza R.I.D.,
RA Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011820; AAM36735.1; -
KW Complete proteome.
SQ SEQUENCE 415 AA; 47385 MW; B527492E96CE6811 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 415;
Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 23 AQLDALL 29
DB 284 AQLDALL 290
[1]_taxID=92829;

RESULT 39
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9R6TO
D QSR6TO PRELIMINARY; PRT; 456 AA.
C QSR6TO;
Y 01-MAY-2000 (TrEMBLrel. 13, Created)
Y 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Y 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Ccs1.
N Ccs1.
S Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
C Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
X NCBI_TaxID=1139;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=PCC 6301;
X MEDLINE=91271233; PubMed=1905010;
A Tsinozemas N.F., Castets A.M., Harrison M.A., Allen J.F.,
A Tandeau de Marsac N.;
T "Photosynthetic electron transport controls nitrogen assimilation in
T cyanobacteria by means of posttranslational modification of the glnB
T gene product.";
L Proc. Natl. Acad. Sci. U.S.A. 88:4565-4569(1991).
N [2]
P SEQUENCE FROM N.A.
C STRAIN=PCC 6301;
A Inoue K., Bryant D.A.;
T "Genes required for c-type cytochrome biogenesis.";
L Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
R EMBL; AF079137; AAF04332.1; -.
Q SEQUENCE 456 AA; 50460 MW; 80087557590A22E2 CRC64;

Query Match 5.7%; Score 7; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 21 VLAQLDA 27
| | | | |
b 439 VLAQLDA 445

RESULT 40
D QXSS9 PRELIMINARY; PRT; 457 AA.
C QXSS9;
Y 01-MAR-2002 (TrEMBLrel. 20, Created)
Y 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Y 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Y Hypothetical transmembrane protein RSP0388.
N RSP0388 OR RS00816.
S Ralstonia solanacearum (Pseudomonas solanacearum).
X Plasmid megaplasmid.
C Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
X Ralstoniaceae; Ralstonia.
X NCBI_TaxID=305;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=GM11000;
X MEDLINE=21681879; PubMed=11823852;
A Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
A Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
A Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
A Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
A Weissenbach J., Boucher C.A.;
T "Genome sequence of the plant pathogen Ralstonia solanacearum.";
L Nature 415:497-502(2002).
N [2]
C STRAIN=CO-92 / Biovar Orientalis;
X MEDLINE=21470413; PubMed=11586360;
A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
A Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
A Fellwell T., Hamlin N., Holroyd S., Jagels K., Kariyasev A.V.,
A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
A Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
T "Genome sequence of Yersinia pestis, the causative agent of plague.";

Query Match 5.7%; Score 7; DB 16; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LAQLDAL 28
| | | | |
Db 374 LAQLDAL 380

RESULT 41
QSRVH5 PRELIMINARY; PRT; 462 AA.
C QSRVH5;
Y 01-MAY-2000 (TrEMBLrel. 13, Created)
Y 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Y 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Kynureninase, putative.
GN D5A0338.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
X NCBI_TaxID=1299;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=R1;
X MEDLINE=20036896; PubMed=10567266;
A White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
A Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
A Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
A Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
A Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
A Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
A Fraser C.M.;
T "Genome sequence of the radioresistant bacterium Deinococcus
T radiodurans R1.";
R Science 286:1571-1577(1999).
DR EMBL; AE001863; AAF12444.1; -.
DR TIGR; DRA0338; -.
KW Complete proteome.
SQ SEQUENCE 462 AA; 49548 MW; E6C5EB37B04F431F CRC64;

Query Match 5.7%; Score 7; DB 16; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LAQLDAL 28
| | | | |
Db 62 LAQLDAL 68

RESULT 42
QSZFF3 PRELIMINARY; PRT; 464 AA.
C QSZFF3;
Y 01-MAR-2002 (TrEMBLrel. 20, Created)
Y 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Y 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative membrane protein (putative transport protein).
GN YP01759 OR Y2549.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
X NCBI_TaxID=632;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=CO-92 / Biovar Orientalis;
X MEDLINE=21470413; PubMed=11586360;
A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
A Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
A Fellwell T., Hamlin N., Holroyd S., Jagels K., Kariyasev A.V.,
A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
A Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
T "Genome sequence of Yersinia pestis, the causative agent of plague.";

Query Match 5.7%; Score 7; DB 16; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1L Nature 413:523-527(2001).
1N [2]
1P SEQUENCE FROM N.A.
1Q STRAIN=KIM5 / Biovar Mediaevalis;
1X MEDLINE=42137863; PubMed=12142430;
1A Deng W., Burland V., Flunkett G. III, Boutin A., Mayhew G.F., Liss P.,
1A Peria N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
1A Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
1A Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
1A Perry R.D.;
1T "Genome sequence of Yersinia pestis KIM.";
1L J. Bacteriol. 194:4601-4611(2002).
1R EMBL; AJ414150; CAC90578.1; -.
1R EMBL; AB013857; AAM86104.1; -.
1R InterPro; IPR000644; CBS domain.
1R InterPro; IPR005170; CorC HlyC.
1R InterPro; IPR005496; TerC.
1R Pfam; PF00571; CBS; 2.
1R Pfam; PF03471; CorC HlyC; 1.
1R Pfam; PF03741; TerC; 1.
1R Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 464 AA; 51095 MW; CEC95AC241112416 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 5 CLSFLM 11
DB 139 CLSFLM 145

RESULT 43
296528 PRELIMINARY; PRT; 468 AA.
AC C94528
AC C94528;
AC C94528;
AC 01-MAY-1999 (TRENBLrel. 10, Created)
AC 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
AC 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
AC Synapse-enriched clathrin adaptor protein LAP.
AC LAP OR BCDA:GM10787 OR CG2520.
AC Drosophila melanogaster (Fruit fly).
AC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
AC Ephydroidea; Drosophilidae; Drosophila.
AC NCBI_TaxID=7227;
AC [1]
AC SEQUENCE FROM N.A.
AC MEDLINE=93098207; PubMed=9883738;
AC Zhang B., Koh Y.H., Beckstead R.B., Budnik V., Ganetzky B.,
AC Bellen H.J.;
AC "Synaptic vesicle size and number are regulated by a clathrin adaptor
AC protein required for endocytosis.";
AC Neuron 21:1465-1475(1998).
AC EMBL; AF075247; AAD08669.1; -.
AC FlyBase; FBgn0026210; lap.
AC InterPro; IPR001026; ENTH.
AC Pfam; PF01417; ENTH; 1.
AC Pfam; PF01417; ENTH; 1.
AC SMART; SM00273; ENTH; 1.
AC SMART; SM00273; ENTH; 1.
AC SEQUENCE 468 AA; 49807 MW; F78D60A559E4CB00 CRC64;

Query Match 5.7%; Score 7; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDALL 29
DB 187 AQLDALL 193

RESULT 44
Q9VI75 PRELIMINARY; PRT; 468 AA.
ID Q9VI75
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AC Q9VI75;
AC 01-MAY-2000 (TRENBLrel. 13, Created)
AC 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
AC 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
AC LAP protein.
AC LAP OR BCDA:GM10787 OR CG2520.
AC Drosophila melanogaster (Fruit fly).
AC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
AC Ephydroidea; Drosophilidae; Drosophila.
AC NCBI_TaxID=7227;
AC [1]
AC SEQUENCE FROM N.A.
AC STRAIN=BERKELEY;
AC MEDLINE=20196006; PubMed=10731132;
AC Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
AC Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
AC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
AC Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
AC Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
AC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
AC April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
AC Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
AC Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
AC Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
AC Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
AC Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
AC de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
AC Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
AC Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
AC Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
AC Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
AC Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
AC Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
AC Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
AC Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
AC Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
AC Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
AC Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
AC Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,
AC Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
AC Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
AC Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
AC Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
AC Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
AC Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
AC Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
AC Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
AC Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
AC "The genome sequence of Drosophila melanogaster.";
AC Science 287:2185-2195(2000).
AC EMBL; AE003672; AAF54050.1; -.
AC FlyBase; FBgn0026210; lap.
AC InterPro; IPR001026; ENTH.
AC Pfam; PF01417; ENTH; 1.
AC SMART; SM00273; ENTH; 1.
AC SMART; SM00273; ENTH; 1.
AC SEQUENCE 468 AA; 49867 MW; 4B3011615AF007A0 CRC64;

Query Match 5.7%; Score 7; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDALL 29
DB 187 AQLDALL 193

RESULT 45
Q9VM1 PRELIMINARY; PRT; 468 AA.
ID Q9VM1
AC Q9VM1;
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01-OCT-2002 (Tremblrel. 22, Created)
 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 RH473959.
 LAP OR BCDNA:GM10787 OR CG2520.
 Drosophila melanogaster (fruit fly).
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=Berkeley;
 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 George R., Gonzalez B., Guarin H., Kronmiller B., Li P., Liao G.,
 Miranda A., Mungall C.J., Nuncio J., Pacleb J., Paragas V., Park S.,
 Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 Celnik S.,
 Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AY128498; AAW75091.1; -
 FlyBase; FBgn0026210; lap.
 InterPro; IPR001026; ENTH.
 Pfam; PF01417; ENTH; 1.
 SMART; SMO0273; ENTH; 1.
 SEQUENCE 468 AA; 49819 MW; FF5B7CD62C5DADC3 CRC64;
 Query Match 5.7%; Score 7; DB 5; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 23 AQLDALL 29
 187 AQLDALL 193
 RESULT 46
 Q9H0W0 PRELIMINARY; PRT; 484 AA.
 Q9H0W0;
 01-MAR-2001 (Tremblrel. 16, Created)
 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 VNG0983C.
 VNG0983C.
 Halobacterium sp. (strain NRC-1).
 Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
 Halobacteriaceae; Halobacterium.
 NCBI_TaxID=64091;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=20504493; PubMed=11016950;
 NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 Shukla H.D., Laaky S.R., Balliga N.S., Thorsson V., Sbrogna J.,
 Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 Isenbarger T.A., Peck R.F., Pohlschroder M., Spidich J.L., Jung K.-H.,
 Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Oner A.D.,
 Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 "Genome sequence of Halobacterium species NRC-1";
 Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 EMBL; AE005034; AAG19401.1; -
 InterPro; IPR000205; NAD binding.
 InterPro; IPR001667; Phosphatase.
 InterPro; IPR003148; TPKA_N.
 Pfam; PF01368; DHH; 1.
 Pfam; PF02254; TPKA; 1.
 Complete proteome.
 SEQUENCE 484 AA; 51978 MW; E511C596BF8007E7 CRC64;
 Query Match 5.7%; Score 7; DB 17; Length 484;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LSVSQT 21
 DB 287 LSVSQT 293
 RESULT 47
 Q8ZP05 PRELIMINARY; PRT; 518 AA.
 Q8ZP05;
 01-MAR-2002 (Tremblrel. 20, Created)
 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 Putative inner membrane protein.
 YOAE OR STM1828.
 Salmonella typhimurium.
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Salmonella.
 NCBI_TaxID=602;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=LT2 / SGSC1412 / ATCC 700720;
 MEDLINE=21534948; PubMed=11677609;
 McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 Waterston R., Wilson R.K.;
 "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2";
 Nature 413:852-856(2001).
 EMBL; AE008781; AAL20743.1; -
 InterPro; IPR000644; CBS domain.
 InterPro; IPR005170; CorC_HlyC.
 InterPro; IPR005496; TerC.
 Pfam; PF00571; CBS; 2.
 Pfam; PF03471; CorC_HlyC; 1.
 Pfam; PF03741; TerC; 1.
 SMART; SMO0116; CBS; 2.
 KW Hypothetical protein; Complete proteome.
 SEQUENCE 518 AA; 56346 MW; D05DF6DD0106EAS CRC64;
 Query Match 5.7%; Score 7; DB 16; Length 518;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CLSFLM 11
 DB 189 CLSFLM 195
 RESULT 48
 Q8Z674 PRELIMINARY; PRT; 519 AA.
 Q8Z674;
 01-MAR-2002 (Tremblrel. 20, Created)
 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 Putative membrane protein.
 STY1958.
 Salmonella typhi.
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Salmonella.
 NCBI_TaxID=601;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=CT18;
 MEDLINE=21534947; PubMed=11677608;
 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

JA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
JA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
JA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
JA Whitehead S., Barrell B.G.,
JA "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
KT Nature 413:848-852(2001).
LT EMBL; AL627272; CAD05811.1; -;
RR InterPro; IPR000644; CBS domain.
RR InterPro; IPR005170; CorC_HlyC.
RR InterPro; IPR005496; TerC.
RR Pfam; PF00571; CBS; 2.
RR Pfam; PF03471; CorC_HlyC; 1.
RR Pfam; PF03741; TerC; 1.
RR SMART; SM00116; CBS; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 519 AA; 56523 MW; 68918E845E3087 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 519;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 5 CLSFLM 11
2b 189 CLSFLM 195

RESULT 49
2b2NQ8 PRELIMINARY; PRT; 526 AA.
ID Q8ZKQ8;
AC Q8ZKQ8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative inner membrane protein.
GN YEGH OR STW2119.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Bante M., Du F., Hong S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RT Nature 413:852-856(2001).
RL EMBL; AF008794; AAL21023.1; -;
DR InterPro; IPR000644; CBS domain.
DR InterPro; IPR005170; CorC_HlyC.
DR InterPro; IPR005496; TerC.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF03471; CorC_HlyC; 1.
DR Pfam; PF03741; TerC; 1.
DR SMART; SM00116; CBS; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 526 AA; 58973 MW; 3BD4B0E40DA6F3EF CRC64;

Query Match 5.7%; Score 7; DB 16; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLM 11
Db 189 CLSFLM 195

RESULT 50

Q8Z5G3 PRELIMINARY; PRT; 526 AA.
ID Q8Z5G3;
AC Q8Z5G3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative membrane protein.
GN YEGH OR STY2332.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RT Nature 413:848-852(2001).
RL EMBL; AL627273; CAD02482.1; -;
DR InterPro; IPR000644; CBS domain.
DR InterPro; IPR005170; CorC_HlyC.
DR InterPro; IPR005496; TerC.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF03471; CorC_HlyC; 1.
DR Pfam; PF03741; TerC; 1.
DR SMART; SM00116; CBS; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 526 AA; 59003 MW; 8FD4A24177C33F5 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLM 11
Db 189 CLSFLM 195

RESULT 51
Q8XQP9 PRELIMINARY; PRT; 526 AA.
ID Q8XQP9;
AC Q8XQP9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Probable transmembrane protein.
GN RSP1172 OR RS05062.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Denange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RT Nature 415:497-502(2002).
RL

R EMBL; AL646083; CAD19323.1; -;
R InterPro; IPR000644; CBS domain.
R InterPro; IPR005170; CorC HlyC.
R InterPro; IPR005496; Terc.
R Pfam; PF00571; CBS; 2.
R Pfam; PF03471; CorC HlyC; 1.
R Pfam; PF03741; Terc; 1.
W Plasmid; Complete proteome.
Q SEQUENCE 526 AA; 5719 MW; 4B0D7B20F561A22 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 5 CLSFLIM 11
b 189 CLSFLIM 195

RESULT 52
8ZF26 PRELIMINARY; PRT; 528 AA.
D Q8ZF26
C Q8ZF26; 20, Created)
T 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
T 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
E Putative membrane protein.
N YPO1527.
S Yersinia pestis.
C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
C Enterobacteriaceae; Yersinia.
X NCBI_TaxID=632;
[1]
SEQUENCE FROM N.A.
C STRAIN=CO-92 / Biovar Orientalis;
X MEDLINE=21470413; PubMed=11586350;
A Parkhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
A Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
A Leather S., Moulton P.C.F., Quail M., Rutherford K.,
A Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
T "Genome sequence of Yersinia pestis, the causative agent of plague."
L Nature 413:523-527(2001).
R EMBL; AJ414148; CAC90350.1; -;
R InterPro; IPR000644; CBS domain.
R InterPro; IPR005170; CorC HlyC.
R InterPro; IPR005496; Terc.
R Pfam; PF00571; CBS; 2.
R Pfam; PF03471; CorC HlyC; 1.
R Pfam; PF03741; Terc; 1.
R SMART; SM00116; CBS; 2.
W Hypothetical protein; Complete proteome.
Q SEQUENCE 528 AA; 59267 MW; 80BFDD245D58568F CRC64;

Query Match 5.7%; Score 7; DB 16; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 5 CLSFLIM 11
b 189 CLSFLIM 195

RESULT 53
8D075 PRELIMINARY; PRT; 537 AA.
C Q8D075
D Q8D075; 23, Created)
T 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
T 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
E Putative membrane protein.

GN Y2643.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Ferns N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.D., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013866; RAM96196.1; -;
SQ SEQUENCE 537 AA; 60323 MW; F787C0D811CF81EC CRC64;

Query Match 5.7%; Score 7; DB 16; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLIM 11
Db 189 CLSFLIM 195

RESULT 54
Q8X7L8 PRELIMINARY; PRT; 549 AA.
ID Q8X7L8
AC Q8X7L8; 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative transport protein.
GN YVGH OR Z3229 OR ECS2868.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 050952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kunara S., Shiba T., Hattori M., Shinagawa H.,
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005432; AAG57123.1; -;
DR EMBL; AP002560; BAB36291.1; -;
DR InterPro; IPR000644; CBS domain.
DR InterPro; IPR005170; CorC HlyC.
DR InterPro; IPR005496; Terc.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF03471; CorC HlyC; 1.
DR Pfam; PF03741; Terc; 1.
DR SMART; SM00116; CBS; 2.

W Complete proteome.
Q SEQUENCE 549 AA; 62077 MW; 2A300AFCA60FD6BF CRC64;
Query Match 5.7%; Score 7; DB 16; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 5 CLSFLM 11
b 211 CLSFLM 217
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RESULT 55
ID Q9U203 PRELIMINARY; PRT; 549 AA.
AC Q9U203;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein yegh.
GN YEGH OR C2590.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:HI / CFT073 / ATCC 700928;
RA MEDLINE=22388234; PubMed=124711157;
XA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
YA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
ZA Mayhew G.P., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
XA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016763; AA81046.1; -;
KW Hypothetical protein; Complete proteome.
Q SEQUENCE 549 AA; 62057 MW; C4C18FCA60FD6B5 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 5 CLSFLM 11
b 211 CLSFLM 217
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RESULT 56
ID Q9U203 PRELIMINARY; PRT; 553 AA.
AC Q9U203;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Y57G11C.9a protein.
GN Y57G11C.9 OR Y57G11C.9A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RA Science 282:2012-2018 (1998).

DR EMBL; Z99281; CAB54457.1; -;
DR WormPep; Y57G11C.9a; CE24476.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
SQ SEQUENCE 553 AA; 63571 MW; A7F22D32D8B9C36 CRC64;

Query Match 5.7%; Score 7; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QLDALLV 30
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DB 545 QLDALLV 551
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RESULT 57
ID Q9SNV7 PRELIMINARY; PRT; 558 AA.
AC Q9SNV7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Pe0 katanin.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99329821; PubMed=10401578;
RA Lochret T.A., Zhao L., Quarby L.M.;
RT "Cloning of Chlamydomonas pe0 katanin and localization to the site of
outer doublet severing during deflagellation.";
RL Cell Motil. Cytoskeleton 43:221-231 (1999).
DR EMBL; AF205377; AAF12877.1; -;
DR InterPro; IPR003593; AAA_Atpase.
DR InterPro; IPR003593; AAA_Atpase_cent.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
KW ATP-binding.
SQ SEQUENCE 558 AA; 60144 MW; 7A9DCCT8F7C028AB CRC64;

Query Match 5.7%; Score 7; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RAGSAPR 66
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DB 182 RAGSAPR 198
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RESULT 58
ID P91720 PRELIMINARY; PRT; 614 AA.
AC P91720;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Decapentaplegic protein.
GN DPP.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9725212; PubMed=9071585;
RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,

LA de Cuevas M., Gelbart W.M.;
 IT "Molecular evolution at the decapentaplegic locus in Drosophila."
 IL Genetics 145:297-305(1997).
 IC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 RR EMBL; U63855; AAC47555.1; -.
 RR HSP; P12643; 3BMP.
 RR FlyBase; FBgn0013109; Dvir\dpp.
 RR InterPro; IPR002405; Inhibin_alpha.
 RR InterPro; IPR001839; TGFb.
 RR InterPro; IPR001111; TGFb_N.
 RR Pfam; PF00019; TGF-beta; 1.
 RR Pfam; PF00688; TGFp_propeptide; 1.
 RR PRINTS; PR00669; INHIBIN.
 RR ProDom; PD000357; TGFb; 1.
 RR SMART; SM00204; TGFb; 1.
 RR PROSITE; PS00250; TGF_BETA_1; 1.
 IQ SEQUENCE 614 AA; 65055 MW; D0F20A4093403DCP CRC64;

Query Match 5.7%; Score 7; DB 5; Length 614;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NY 15 LSVSQTQV 21
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 b 360 LSVSQTQV 366

RESULT 59
 Q9U202 PRELIMINARY; PRT; 659 AA.
 ID Q9U202;
 AC Q9U202;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 IT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Y57G11C.9b protein.
 DE Y57G11C.9 OR Y57G11C.9B.
 CS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 CX NCBI_TaxID=6239;
 [1]
 IP SEQUENCE FROM N.A.
 LA McMurray A.A.;
 IL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 IN [2]
 IN SEQUENCE FROM N.A.
 IX MEDLINE=99069613; PubMed=9851916;
 LA none;
 IT "Genome sequence of the nematode C.elegans: A platform for
 IT investigating biology."
 IL Science 282:2012-2018(1998).
 RR EMBL; Z99281; CAB54458.1; -.
 RR WormPep; Y57G11C.9b; CE24477.
 RR InterPro; IPR000504; RNA_rec_mot.
 RR Pfam; PF00076; rim; 1.
 RR SMART; SM00360; RRM; 1.
 RR PROSITE; PS50102; RRM; 1.
 IQ SEQUENCE 659 AA; 74740 MW; 8FC6694B17D98989 CRC64;

Query Match 5.7%; Score 7; DB 5; Length 659;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NY 24 QLDALLV 30
 |||||
 b 651 QLDALLV 657

RESULT 60
 Q8WPL5 PRELIMINARY; PRT; 689 AA.
 ID Q8WPL5
 AC Q8WPL5;
 IT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Similar to wasp protein (Fragment).
 GN BAC00119.
 OS Oikopleura dioica.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
 OC Oikopleuridae; Oikopleura.
 OX NCBI_TaxID=34765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ste H.C., Kube M., Edvardsen R.B., Jensen M.F., Beck A., Spriet E.,
 RA Gorsky G., Thompson E.M., Lehrach H., Reinhardt R., Chourrout D.;
 RT "The marine chordate Oikopleura dioica has a miniature genome."
 RL Science 0:0-0(2001).
 DR EMBL; AF374376; AAL56445.1; -.
 FT NON_TER 1
 SQ SEQUENCE 689 AA; 76360 MW; D4ECE941408B404F CRC64;

Query Match 5.7%; Score 7; DB 5; Length 689;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LTISPQV 106
 |||||
 Db 318 LTISPQV 324

RESULT 61
 Q8G412 PRELIMINARY; PRT; 701 AA.
 ID Q8G412;
 AC Q8G412;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 IT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein with similarity to z5950 product of Escherichia
 DE coli O157:H7.
 GN BL1400.
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=NCC 2705;
 RX MEDLINE=22294977; PubMed=12381787;
 RA Scheil M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
 RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
 RA Pidmore R.D., Arigoni F.;
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 RT to the human gastrointestinal tract."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 DR EMBL; AE014770; AAN25199.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 701 AA; 79712 MW; 2927BB3B4D002446 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 701;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QLDALLV 30
 |||||
 Db 100 QLDALLV 106

RESULT 62
 Q993H5 PRELIMINARY; PRT; 828 AA.
 ID Q993H5
 AC Q993H5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 IT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE ORF35.
 OS Callitriche herpesvirus 3.

DR Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
DR Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
DR Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
DR Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
DR Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
DR Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
DR Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
DR Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
DR de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
DR Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
DR Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
DR Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
DR Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
DR Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
DR Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
DR Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
DR Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
DR Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
DR Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
DR Merkulov G., Mishina N.V., Mobarly C., Morris J., Moshrefi A.,
DR Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
DR Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
DR Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
DR Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
DR Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
DR Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
DR Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
DR Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
DR Williams S.M., Woodage T., Worley K.C., Wu D., Yang S.-Q., Yao Q.A.,
DR Ye J., Yeh R.-F., Zaveri J., Zhan M., Zhang G., Zhao Q., Zheng L.,
DR Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
DR Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
DR "The genome sequence of *Drosophila melanogaster*.";
DR SEQUENCE 287:2185-2195(2000).
DR [2]
DR SEQUENCE FROM N.A.
DR Celisner S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
DR Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
DR Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
DR Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
DR Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Parfan D.,
DR Periera S., Frise E., Galle R.F., Garg N.S., George R.A.,
DR Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
DR Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
DR McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
DR Pacleb J., Paragass V., Park S., Patel S., Pfeiffer B.,
DR Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
DR Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
DR Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
DR "Sequencing of *Drosophila melanogaster* genome.";
DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR [3]
DR SEQUENCE FROM N.A.
DR Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
DR Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
DR Tupy J.L., Bergman C., Berman B., Carlson J.W., Celisner S.E.,
DR Klomp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
DR Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
DR Searle S.M.J., Smith E., Shu S., Smtiak F., Whitfield E.,
DR Ashburner M., Gelbart W.M., Rubin G.M., Murgall C.J., Lewis S.E.;
DR "Annotation of *Drosophila melanogaster* genome.";
DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR [4]
DR SEQUENCE FROM N.A.
DR Adams M.D., Celisner S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR [5]
DR SEQUENCE FROM N.A.
DR FlyBase;
DR Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003560; AAP50600.2;
DR FlyBase; FBN0052387; CG32387.
DR InterPro; IPR003962; FNIII_subd.

DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00047; ig; 7.
DR PRINIS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00409; IG; 9.
DR SMART; SM00408; IGC2; 9.
DR PROSITE; PS00835; IG LIKE; 9.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 1765 AA; 193274 MW; 81A6A498A903E905 CRC64;

Query Match 5.7%; Score 7; DB 5; Length 1765;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LTISPQV 106
DB 540 LTISPQV 546
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RESULT 66
Q9VS29 PRELIMINARY; PRT; 1770 AA.
ID Q9VS29
AC Q9VS29
DT 01-MAY-2000 (TrEMBLrel_13, Created)
DT 01-OCT-2002 (TrEMBLrel_22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel_23, Last annotation update)
DE CG32387 protein.
GN CG32387 OR CG8618 OR CG8619 OR CG14828.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

A Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
A Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
A Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
A Chan M.-S., Nene V., Shalim S.J., Suh B., Peterson J., Anguoli S.,
A Pertea M., Allen J., Selengut J., Hatt D., Mather M.W., Vaidya A.B.,
A Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
A McFadden G.I., Cummings I.M., Subramanian G.M., Mungall C.,
A Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
A Fraser C.M., Barrall B.,
T "Genome sequence of the human malaria parasite Plasmodium
T falciparum.";
L Nature 419:498-511(2002).
R ENBL; AB001402; AAC71900.2; -.
W Hypothetical protein.
Q SEQUENCE 4091 AA; 494204 MW; 9E98BF6123BB976A CRC64;

Query Match 5.7%; Score 7; DB 5; Length 4091;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 4 RCLSFL 10
b 990 RCLSFL 996

RESULT 69
ID Q9NR17 PRELIMINARY; PRT; 21 AA.
AC Q9NR17
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Pancreatic polypeptide-2.
GN PP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Herzog H., Couzens M., Liu M.;
RL "Peptide YY-2 (PPY2) and pancreatic polypeptide-2 (PPY2): Species
RL specific evolution of novel members of the neuropeptide Y gene
RL family."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL ENBL; AF222903; AAF73875.1; -.
RL Genew; HGNC:9328; PPY2.
SQ SEQUENCE 21 AA; 2179 MW; 2F23E50FF18EBF7D CRC64;

Query Match 4.9%; Score 6; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 ACRLS 7
b 4 ACRLS 9

RESULT 70
ID Q28453 PRELIMINARY; PRT; 43 AA.
AC Q28453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Alpha A-crystallin (Fragment).
DE Leontopithecus rosalia (Golden lion tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Leontopithecus.
OX NCBI_TaxID=30588;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=96139023; PubMed=8587135;
RA Jaworski C.J.;
RT "A reassessment of mammalian alpha A-crystallin sequences using DNA
RT sequencing: implications for anthropoid affinities of tarsier.";
RL J. Mol. Evol. 41:901-908(1995).
DR EMBL; U24067; AAA97569.1; -.
DR InterPro; IPR001436; Crystallin_alpha.
DR InterPro; IPR002068; Hsp20.
DR Pfam; PF00011; HSP20; 1.
DR PRINTS; PR00299; ACRYSTALLIN.
FT NON_TER 1 43
FT NON_TER 43 43
SQ SEQUENCE 43 AA; 4444 MW; 6AC18572EBBCCF5F CRC64;

Query Match 4.9%; Score 6; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 38 LSCTLS 43
b 9 LSCTLS 14

RESULT 71
ID Q9U447 PRELIMINARY; PRT; 56 AA.
AC Q9U447
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Culmination specific protein 45D.
GN 45D.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Loughran G.F., Pinter K., Gross J.D.;
RL "Culmination specific mRNA."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF203735; AAF20921.1; -.
SQ SEQUENCE 56 AA; 6411 MW; BBFED54797DB37A0 CRC64;

Query Match 4.9%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 38 LSCTLS 43
b 34 LSCTLS 39

RESULT 72
ID Q96829 PRELIMINARY; PRT; 56 AA.
AC Q96829
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE Polyprotein (Fragment).
DE Hepatitis A virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Hepatovirus.
OX NCBI_TaxID=12092;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=406909;
RX MEDLINE=97247817; PubMed=9093940;
RA Taylor M.B.;
RT "Molecular epidemiology of South African strains of hepatitis A virus:
RL 1982-1996."
RL J. Med. Virol. 51:273-279(1997).

NR EMBL; U68691; AAB53587.1; -;
RR InterPro; IPR000886; ER target.
RT PROSITE; PS00014; ER TARGET; 1.
TT NON TER 1
TT NON TER 56
TT NON TER 56
TT SEQUENCE 56 AA; 6623 MW; A917151846AEF4A7 CRC64;

Query Match 4.9%; Score 6; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 72 RSEDDH 77
|||
20 RSEDDH 25

RESULT 73

8BTJT4 PRELIMINARY; PRT; 61 AA.
AC 8BTJT4
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE DNA-directed RNA polymerase, subunit E2.
EN RPOE2 OR MA3693.
DS Methanosarcina acetivorans.
DC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
DC Methanosarcinaceae; Methanosarcina.
XX NCBI_TaxID=2214;
XX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=1932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Maylor J., Spange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Firrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Kuetner D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011078; AAM07048.1; -;
KW DNA-directed RNA polymerase; Complete proteome.
SQ SEQUENCE 61 AA; 6844 MW; 5BBAD76E187E8473 CRC64;

Query Match 4.9%; Score 6; DB 17; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRF 87
|||
51 DIPDRF 56

RESULT 74

8BPZ97 PRELIMINARY; PRT; 61 AA.
AC 8BPZ97
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE DNA-directed RNA polymerase subunit E' (EC 2.7.7.6).
GN NM0597.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
XX NCBI_TaxID=2209;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22125824; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wieser A., Baumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea."
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013284; AAM30293.1; -;
KW DNA-directed RNA polymerase; Transferase; Nucleotidyltransferase;
Complete proteome.
SQ SEQUENCE 61 AA; 6881 MW; E54AD76D1B7E9BA1 CRC64;

Query Match 4.9%; Score 6; DB 17; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRF 87
|||
51 DIPDRF 56

RESULT 75

Q8LRE7 PRELIMINARY; PRT; 64 AA.
AC Q8LRE7
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE B101SE06.12 protein.
GN B101SE06.12.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
clone B1015806."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003197; BAB92211.1; -;
DR Gramene; Q8LRE7; -;
SQ SEQUENCE 64 AA; 7711 MW; BB2744453A4C27CA CRC64;

Query Match 4.9%; Score 6; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 DHRPFA 81
|||
37 DHRPFA 42

Search completed: February 9, 2004, 12:59:05
Job time : 66 secs

GenCore version 5.1.6
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WM protein - protein search, using sw model

run on: February 9, 2004, 12:48:32 ; Search time 47 Seconds
(without alignments)

415.391 Million cell updates/sec

Title: US-09-981-876-200

Perfect score: 123

Sequence: 1 MACRCISFLMTGLSVSQT.....PVQPEDDADYCVSYGVGFSP 123

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	123	100.0	123	19	AAW75123
2	123	100.0	123	21	AAW24061
3	123	100.0	123	21	AAW66655
4	123	100.0	123	22	AAU12372
5	123	100.0	123	22	AAW61178
6	123	100.0	123	24	ABU56770
7	123	100.0	123	24	ABU57046
8	123	100.0	123	24	ABU59851
9	123	100.0	123	24	ABU59071

10	123	100.0	123	24	ABU59218	Human secreted/tra
11	123	100.0	123	24	ABU59367	Novel human secret
12	123	100.0	123	24	ABU60502	Human secreted/tra
13	123	100.0	123	24	ABU57993	Human PRO polypept
14	123	100.0	123	24	ABU58924	Human secreted/tr
15	123	100.0	123	24	ABU13884	Human PRO619 polyp
16	123	100.0	123	24	ABU10839	Human PRO polypept
17	119	96.7	141	22	AAW39690	Human polypeptide
18	107	87.0	113	22	AAW41476	Human polypeptide
19	9	7.3	258	23	ABP45354	Human BlyS binding
20	8	6.5	235	22	AAW38953	Human lung specific
21	8	6.5	246	23	AAW20273	Human novel polype
22	8	6.5	526	23	ABG66690	Human novel polype
23	8	6.5	588	23	ABG66689	Human pif-1 type h
24	8	6.5	689	22	AAE01020	Novel human diagno
25	8	6.5	1249	22	ABG21666	Peptidomimetic ant
26	7	5.7	14	24	ABP76447	Peptidomimetic ant
27	7	5.7	14	24	ABP76448	Human derived ligh
28	7	5.7	103	16	AAW80091	Human T lymphocyte
29	7	5.7	103	20	AAW95489	Human T lymphocyte
30	7	5.7	104	13	AAW26962	Anti-HIV gp120 imm
31	7	5.7	104	15	AAW54313	VL region of HIV n
32	7	5.7	104	17	AAW01271	Anti-gp120 antibod
33	7	5.7	104	21	AAW95123	Anti-gp120 antibod
34	7	5.7	104	21	AAW98232	Novel human diagno
35	7	5.7	105	22	ABG22849	HSV glycoprotein F
36	7	5.7	109	15	AAW50217	Rabbit anti-A33 an
37	7	5.7	109	22	AAW98230	Rabbit anti-A33 an
38	7	5.7	109	22	AAW98231	Rabbit anti-A33 an
39	7	5.7	109	22	AAW98232	Humanised anti-A33
40	7	5.7	109	22	AAW98233	Humanised anti-A33
41	7	5.7	109	22	AAW98234	Humanised anti-A33
42	7	5.7	109	22	AAW98235	Humanised anti-A33
43	7	5.7	109	22	AAW98236	Humanised anti-A33
44	7	5.7	109	22	AAW98237	Humanised anti-A33
45	7	5.7	109	22	AAW98238	Humanised anti-A33
46	7	5.7	109	22	AAW98239	Humanised anti-A33
47	7	5.7	109	22	AAW75149	Rabbit anti A33 an
48	7	5.7	109	22	AAW75150	Rabbit anti A33 an
49	7	5.7	109	22	AAW75151	Humanised rabbit a
50	7	5.7	109	22	AAW75152	Human anti A33 ant
51	7	5.7	109	22	AAW75153	Human anti A33 ant
52	7	5.7	109	22	AAW75154	Human anti A33 ant
53	7	5.7	109	22	AAW75155	Human anti A33 ant
54	7	5.7	109	22	AAW75156	Human anti A33 ant
55	7	5.7	109	22	AAW75157	Human anti A33 ant
56	7	5.7	109	22	AAW75158	Human anti A33 ant
57	7	5.7	111	15	AAW54277	Anti-HIV gp41 immu
58	7	5.7	111	16	AAW69089	Anti-HIV gp41 immu
59	7	5.7	111	17	AAW01322	VL of Fab, GL 41
60	7	5.7	111	18	AAW08738	Human anti-HIV Fab
61	7	5.7	111	21	AAW95172	Anti-gp41 light ch
62	7	5.7	111	21	AAW98281	Anti-gp41 light ch
63	7	5.7	120	23	ABG64978	Human albumin fusi
64	7	5.7	120	23	ABG64980	Human albumin fusi
65	7	5.7	120	23	AAE21465	Human gene 14 enco
66	7	5.7	120	23	AAE21495	Human gene 14 enco
67	7	5.7	121	22	AAU17887	Novel human respir
68	7	5.7	122	22	ABG18228	Novel human diagno
69	7	5.7	161	22	ABG12887	Novel human diagno
70	7	5.7	182	22	ABG19759	Novel human diagno
71	7	5.7	211	22	ABW11775	Human 14274 recept
72	7	5.7	214	18	AAW45517	NANUC-2 light chai
73	7	5.7	214	18	AAW07615	Ulcerative colitis
74	7	5.7	214	19	AAW64671	Human UC PANCA mon
75	7	5.7	214	20	AAW34039	NANUC-2 antibody 1
76	7	5.7	214	21	AAW57337	UC PANCA MAB NANUC
77	7	5.7	223	22	ABG18298	Novel human diagno
78	7	5.7	235	21	AAW15547	Human immune syste
79	7	5.7	243	23	ABP45852	Human BlyS binding
80	7	5.7	244	23	ABG19289	Novel human diagno
81	7	5.7	245	23	ABP45855	Human BlyS binding
82	7	5.7	251	23	ABP45490	Human BlyS binding

83	7	5.7	257	23	ABP45241	Human Blys binding
84	7	5.7	259	23	ABP45266	Human Blys binding
85	7	5.7	255	24	ABJ18943	Pathogen specific
86	7	5.7	270	21	ABK32538	S. lavendulae Mit
87	7	5.7	277	22	ABG19760	Novel human diagno
88	7	5.7	307	23	ABP27372	Streptococcus poly
89	7	5.7	307	23	AAU77622	S. agalactiae extr
90	7	5.7	317	22	ACG93163	C glutamicum prote
91	7	5.7	322	21	ACG39031	Arabidopsis thalia
92	7	5.7	371	23	AB555164	Lactococcus lactis
93	7	5.7	413	22	ABG09223	Novel human diagno
94	7	5.7	419	24	ABF79933	N. gonorrhoeae ami
95	7	5.7	419	24	ABP80542	N. gonorrhoeae ami
96	7	5.7	468	22	ABB59169	Drosophila melanog
97	7	5.7	597	22	ABG06708	Novel human diagno
98	7	5.7	597	22	ABG26819	Novel human diagno
99	7	5.7	848	22	ABG25748	Novel human diagno
100	7	5.7	934	16	AA876063	Human MSH2 protein

ALIGNMENTS

RESULT 1
AAW75123 standard; Protein; 123 AA.
AC AAW75123;
XT 25-MAR-2003 (updated)
XT 28-JAN-1999 (first entry)
DE Human secreted protein encoded by gene 67 clone HRGDF73.

Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; retinosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; cecsis; lung; thyroiditis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.
XX WO9839446-A2.
XX 11-SEP-1998.

XX 06-MAR-1998; 98WO-US04482.
XX 07-MAR-1997; 97US-0038621.
XX 07-MAR-1997; 97US-0040161.
XX 07-MAR-1997; 97US-0040162.
XX 07-MAR-1997; 97US-0040163.
XX 07-MAR-1997; 97US-0040333.
XX 07-MAR-1997; 97US-0040334.
XX 07-MAR-1997; 97US-0040336.
XX 07-MAR-1997; 97US-0040626.
XX 11-APR-1997; 97US-0043311.
XX 11-APR-1997; 97US-0043312.
XX 11-APR-1997; 97US-0043313.
XX 11-APR-1997; 97US-0043314.
XX 11-APR-1997; 97US-0043315.
XX 11-APR-1997; 97US-0043568.
XX 11-APR-1997; 97US-0043569.
XX 11-APR-1997; 97US-0043576.
XX 11-APR-1997; 97US-0043578.
XX 11-APR-1997; 97US-0043580.
XX 11-APR-1997; 97US-0043669.
XX 11-APR-1997; 97US-0043670.
XX 11-APR-1997; 97US-0043671.
XX 11-APR-1997; 97US-0043672.

PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0058630.
PR 22-AUG-1997; 97US-0058631.
PR 22-AUG-1997; 97US-0058632.
PR 22-AUG-1997; 97US-0058636.
PR 22-AUG-1997; 97US-0058637.
PR 22-AUG-1997; 97US-0058662.
PR 22-AUG-1997; 97US-0058664.
PR 22-AUG-1997; 97US-0058845.
PR 22-AUG-1997; 97US-0058862.
PR 22-AUG-1997; 97US-0058864.
PR 22-AUG-1997; 97US-0058872.
PR 22-AUG-1997; 97US-0058874.
PR 22-AUG-1997; 97US-0058875.
PR 22-AUG-1997; 97US-0058876.
PR 22-AUG-1997; 97US-0058877.
PR 22-AUG-1997; 97US-0058878.
PR 22-AUG-1997; 97US-0058879.
PR 22-AUG-1997; 97US-0058880.
PR 22-AUG-1997; 97US-0058881.
PR 22-AUG-1997; 97US-0058882.
PR 22-AUG-1997; 97US-0058884.
PR 22-AUG-1997; 97US-0058886.
PR 22-AUG-1997; 97US-0058887.
PR 22-AUG-1997; 97US-0058888.
PR 22-AUG-1997; 97US-0058889.
PR 22-AUG-1997; 97US-0058892.
PR 22-AUG-1997; 97US-0058893.
PR 22-AUG-1997; 97US-0058894.
PR 22-AUG-1997; 97US-0058903.
PR 22-AUG-1997; 97US-0058908.
PR 22-AUG-1997; 97US-0058909.
PR 22-AUG-1997; 97US-0058910.
PR 22-AUG-1997; 97US-0058911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057761.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA

X I Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC, Bednarik DP;
 X II Endress CA, Yu G, Ni J, Peng P, Young PE, Greene JM, Ferrie AM;
 X III Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 X IV Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 X R WPI; 1998-609887/51.
 X R N-PSDB; AAV34220.
 X R X
 X T New isolated human genes and the secreted polypeptides they encode
 X T - useful for diagnosis and treatment of e.g. cancers, neurological
 X T disorders, immune diseases, inflammation or blood disorders
 X S Claim 1; Page 320-321; 447pp; English.
 X C This sequence represents a secreted human protein encoded by the gene
 X C clone detailed in the descriptor line.
 X C The gene can be used to generate fusion proteins by linking to the gene
 X C to a human immunoglobulin Fc portion (e.g. AAV34145) for increasing the
 X C stability of the fused protein as compared to the human protein only.
 X C The invention relates to 70 novel genes and their fragments (nucleic
 X C acid sequences: AAV34154-V34276; amino acid sequences AAV75057-W75179)
 X C which are useful for preventing, treating or ameliorating medical
 X C conditions e.g. by protein or gene therapy. Also, pathological
 X C conditions can be diagnosed by determining the amount of the new
 X C polypeptides in a sample or by determining the presence of mutations in
 X C the new polynucleotides. Specific uses are described for each of the 70
 X C polynucleotides, based on which tissues they are most highly expressed in
 X C (see AAV34154 for described uses).
 X C (Updated on 25-MAR-2003 to correct PF field.)
 X C (Updated on 25-MAR-2003 to correct PI field.)
 X Q Sequence 123 AA;

Query Match 100.0%; Score 123; DB 19; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4.8e-117; Gaps 0;
 Matches 123; Conservative 0; Mismatches 0; Indels 0;
 Y 1 MACRCLSFLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGSWYQQR 60
 b 1 MACRCLSFLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGSWYQQR 60
 Y 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYCVSYG 120
 b 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYCVSYG 120
 Y 121 FSP 123
 b 121 FSP 123

RESULT 2
 VAB24061
 ID AAB24061 standard; Protein; 123 AA.
 CX AAB24061;
 CX 29-JAN-2001 (first entry)
 CX Human PRO619 protein sequence SEQ ID NO:16.
 CX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 CX Proliferation; tumorigenesis; identification; cancer; cytostatic;
 CX immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 CX neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
 CX hypothalamic disorder; glandular disorder; macrophagal disorder;
 CX epithelial disorder; stromal disorder; blastocoealic disorder;
 CX inflammatory disorder; immunologic disorder.
 CX Homo sapiens.
 CX WO200053755-A2.

XX 14-SEP-2000.
 PD 06-JAN-2000; 2000WO-US00376.
 PF 08-MAR-1999; 99WO-US05028.
 XX 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 30-NOV-1999; 99WO-US28313.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 XX Watanabe CK, Wood MI;
 PI WPI; 2000-572270/53.
 XX N-PSDB; AAC58371.
 DR Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 XX treatment, diagnosis and prevention of cancer -
 PT Claim 61; Fig 10; 286pp; English.
 XX The present invention describes an isolated antibody that binds to
 XX one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO1293, PRO339, PRO834, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds may be used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
 CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoealic disorders, and inflammatory,
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.
 XX Sequence 123 AA;

Query Match 100.0%; Score 123; DB 21; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4.8e-117;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MACRCLSFLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGSWYQQR 60
 DB 1 MACRCLSFLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGSWYQQR 60
 QY 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYCVSYG 120
 DB 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYCVSYG 120
 QY 121 FSP 123
 DB 121 FSP 123
 RESULT 3
 AAY66655
 ID AAY66655 standard; protein; 123 AA.

XX AC AAY66655;
XX DT 05-APR-2000 (first entry)
XX DE Membrane-bound protein PRO619.
XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX CS Homo sapiens.
XX PN WO9963088-A2.
XX PD 09-DEC-1999.
XX PF 02-JUN-1999; 99WO-US12252.
XX 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 18-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090576.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091826.
PR 02-JUL-1998; 98US-0091828.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096881.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 18-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.

26-AUG-1998; 98US-0097974.
 26-AUG-1998; 98US-0097978.
 26-AUG-1998; 98US-0097979.
 26-AUG-1998; 98US-0097986.
 26-AUG-1998; 98US-0098014.
 31-AUG-1998; 98US-0098525.
 16-SEP-1998; 98US-0100634.
 12-JAN-1999; 99US-0115565.
 (GETH) GENENTECH INC.
 Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 Wood WI, Yuan J;
 WPI; 2000-072883/06.
 N-PSDB; AAZ64983.
 Membrane-bound proteins and related nucleotide sequences
 claim 12; Fig 68; 822pp; English.
 The invention provides membrane-bound PRO polypeptides and
 polynucleotides encoding them. The PRO sequences of the invention were
 identified based on extracellular domain homology screening. The PRO
 sequences have homology with proteins including LDL receptors, TIE
 ligands and various enzymes. The membrane-bound proteins and receptor
 molecules are useful as pharmaceutical and diagnostic agents. Receptor
 immunoadhesins, for instance, can be used as therapeutic agents to block
 receptor-ligand interactions. The membrane-bound proteins can also be
 employed for screening of potential peptide or small molecule inhibitors
 of the relevant receptor/ligand interaction. The PRO encoding sequences
 are useful as hybridization probes, in chromosome and gene mapping and in
 the generation of antisense RNA and DNA. PRO nucleic acid sequences
 will also be useful for the preparation of PRO polypeptides, especially
 by recombinant techniques.
 Sequence 123 AA;
 Query Match 100.0%; Score 123; DB 21; Length 123;
 Best Local Similarity 100.0%; Pred. NO. 4.8e-117; Gaps 0;
 Matches 123; Conservative 0; Mismatches 0; Indels 0;
 1 MACRCLFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQQR 60
 1 MACRCLFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQQR 60
 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDPAHNAACVLTISPQPEDDADYCSVG 120
 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDPAHNAACVLTISPQPEDDADYCSVG 120
 121 FSP 123
 121 FSP 123
 RESULT 4
 AAU12372
 ID AAU12372 standard; Protein; 123 AA.
 AAU12372;
 24-OCT-2001 (first entry)
 Human PRO619 polypeptide sequence.
 Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 adipocyte; A-peptide; factor VIIA; gene therapy.
 Homo sapiens.
 WO200140466-A2.

07-JUN-2001.
 01-DEC-2000; 2000WO-US32678.
 01-DEC-1999; 99WO-US28301.
 01-DEC-1999; 99WO-US28634.
 02-DEC-1999; 99WO-US28551.
 02-DEC-1999; 99WO-US28564.
 02-DEC-1999; 99WO-US28565.
 09-DEC-1999; 99US-0170262.
 16-DEC-1999; 99WO-US30095.
 20-DEC-1999; 99WO-US30911.
 20-DEC-1999; 99WO-US30999.
 30-DEC-1999; 99WO-US31243.
 06-JAN-2000; 2000WO-US00277.
 06-JAN-2000; 2000WO-US00376.
 11-FEB-2000; 2000WO-US03565.
 18-FEB-2000; 2000WO-US04341.
 18-FEB-2000; 2000WO-US04342.
 22-FEB-2000; 2000WO-US04414.
 24-FEB-2000; 2000WO-US04914.
 24-FEB-2000; 2000WO-US05004.
 01-MAR-2000; 2000WO-US05601.
 20-MAR-2000; 2000WO-US07377.
 21-MAR-2000; 2000WO-US07532.
 30-MAR-2000; 2000WO-US08439.
 17-MAY-2000; 2000WO-US13705.
 22-MAY-2000; 2000WO-US14042.
 30-MAY-2000; 2000WO-US14941.
 02-JUN-2000; 2000WO-US15264.
 10-NOV-2000; 2000WO-US30873.
 (GETH) GENENTECH INC.
 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski FJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 WPI; 2001-408281/43.
 N-PSDB; AAS21444.
 Isolated, secretory and transmembrane PRO polypeptide used to detect
 other PRO polypeptides, link bioactive molecules to cells expressing
 PRO polypeptides, and detect the presence of mammalian tumours e.g.
 lung, breast, prostate, cervical
 Claim 12; Fig 402; 813pp; English.
 AAU12172-AAU12446 represent novel human secretory and transmembrane
 PRO polypeptides. The PRO polypeptides are useful to detect other
 PRO polypeptides, to link bioactive molecules to cells expressing
 PRO polypeptides, to modulate biological activities of cells expressing
 PRO polypeptides, and to detect the presence of mammalian lung, colon,
 breast, prostate, rectal, cervical or liver tumours by comparing PRO
 polypeptide expression in a cell sample to that in a control sample.
 Some of the 275 sequences are also useful to stimulate the release of
 tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 proliferation or differentiation of chondrocytes, the proliferation or
 gene expression in pericyte cells, the release of proteoglycans from
 cartilage, the proliferation of inner ear utricular supporting cells or
 of T-lymphocytes, the release of a cytokine from peripheral blood
 monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 the PRO polypeptides may modulate glucose or free fatty acid uptake by
 skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 to factor VIIA. The PRO polypeptides can be used in assays to identify
 molecules involved in binding interactions. The polynucleotides encoding
 PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 transgenic or knock out animals and can be used in gene therapy.
 Sequence 123 AA;
 Query Match 100.0%; Score 123; DB 22; Length 123;

Best Local Similarity 100.0%; Pred. No. 4.8e-117; Mismatches 0; Indels 0; Gaps 0;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 MACRCISFLMGTFLLSVQTLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
 D 1 MACRCISFLMGTFLLSVQTLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
 Y 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSGVG 120
 D 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSGVG 120
 Y 121 FSP 123
 D 121 FSP 123
 RESULT 5
 AAB65178
 ID AAB65178 standard; Protein; 123 AA.
 AC AAB65178;
 JT 02-APR-2001 (first entry)
 DE Human PRO619 (UNQ355) protein sequence SEQ ID NO:117.
 KW Human; secreted and transmembrane protein; PRO; cytotstatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 KS Homo sapiens.
 X WO2000073454-A1.
 PN 07-DEC-2000.
 PD 30-MAR-2000; 2000WO-US08439.
 PF 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US1090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX WPI; 2001-032160/04.
 DR N-PSDB; AAF44129.

XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX Claim 12; Fig 68; 935pp; English.
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytotstatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX Sequence 123 AA;
 SQ Query Match 100.0%; Score 123; DB 22; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4.8e-117;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MACRCISFLMGTFLLSVQTLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
 Db 1 MACRCISFLMGTFLLSVQTLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
 Qy 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSGVG 120
 Db 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSGVG 120
 Qy 121 FSP 123
 Db 121 FSP 123
 RESULT 6
 AAB66770
 ID AAB66770 standard; Protein; 123 AA.
 AC AAB66770;
 XX 23-MAY-2003 (first entry)
 DE Human PRO polypeptide #201.
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder;
 KW cytotstatic.
 XX Homo sapiens.
 OS US2003036180-A1.
 FN 20-FEB-2003.
 PD 09-MAY-2002; 2002US-0143114.
 PF 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.

R 17-SEP-1998; 99WO-US19437.
R 07-OCT-1998; 99WO-US21141.
R 29-OCT-1998; 99WO-US22991.
R 29-OCT-1998; 99WO-US22992.
R 20-NOV-1998; 99WO-US24855.
R 01-DEC-1998; 99WO-US25108.
R 05-JAN-1999; 99WO-US00106.
R 08-MAR-1999; 99WO-US05028.
R 10-MAR-1999; 99WO-US08190.
R 20-APR-1999; 99WO-US08615.
R 14-MAY-1999; 99WO-US10733.
R 02-JUN-1999; 99WO-US12252.
R 01-SEP-1999; 99WO-US20111.
R 08-SEP-1999; 99WO-US20594.
R 13-SEP-1999; 99WO-US20944.
R 15-SEP-1999; 99WO-US21090.
R 15-SEP-1999; 99WO-US21547.
R 05-OCT-1999; 99WO-US23089.
R 29-NOV-1999; 99WO-US28214.
R 30-NOV-1999; 99WO-US28313.
R 30-NOV-1999; 99WO-US28409.
R 01-DEC-1999; 99WO-US28301.
R 01-DEC-1999; 99WO-US28634.
R 02-DEC-1999; 99WO-US28551.
R 02-DEC-1999; 99WO-US28564.
R 02-DEC-1999; 99WO-US28565.
R 16-DEC-1999; 99WO-US30095.
R 20-DEC-1999; 99WO-US30911.
R 20-DEC-1999; 99WO-US30999.
R 22-DEC-1999; 99WO-US30720.
R 30-DEC-1999; 99WO-US31243.
R 30-DEC-1999; 99WO-US31274.
R 05-JAN-2000; 2000WO-US00219.
R 06-JAN-2000; 2000WO-US00277.
R 06-JAN-2000; 2000WO-US00376.
R 11-FEB-2000; 2000WO-US03565.
R 18-FEB-2000; 2000WO-US04341.
R 18-FEB-2000; 2000WO-US04342.
R 22-FEB-2000; 2000WO-US04414.
R 24-FEB-2000; 2000WO-US04914.
R 01-MAR-2000; 2000WO-US05004.
R 01-MAR-2000; 2000WO-US05601.
R 02-MAR-2000; 2000WO-US05746.
R 02-MAR-2000; 2000WO-US05841.
R 10-MAR-2000; 2000WO-US06319.
R 15-MAR-2000; 2000WO-US06884.
R 20-MAR-2000; 2000WO-US07377.
R 21-MAR-2000; 2000WO-US07532.
R 30-MAR-2000; 2000WO-US08439.
R 17-MAY-2000; 2000WO-US13705.
R 22-MAY-2000; 2000WO-US14042.
R 30-MAY-2000; 2000WO-US14941.
R 02-JUN-2000; 2000WO-US15264.
R 28-JUL-2000; 2000WO-US20710.
R 11-AUG-2000; 2000WO-US22031.
R 23-AUG-2000; 2000WO-US23522.
R 24-AUG-2000; 2000WO-US23328.
R 08-NOV-2000; 2000WO-US30952.
R 10-NOV-2000; 2000WO-US30873.
R 01-DEC-2000; 2000WO-US32678.
R 20-DEC-2000; 2000WO-US34956.
R 28-FEB-2001; 2001WO-US06520.
R 01-MAR-2001; 2001WO-US06566.
R 25-MAY-2001; 2001WO-US17092.
R 01-JUN-2001; 2001WO-US17800.
R 20-JUN-2001; 2001WO-US19692.
R 22-JUN-2001; 2001WO-US20116.
R 29-JUN-2001; 2001WO-US21066.
R 09-JUL-2001; 2001WO-US21735.
R 20-DEC-2000; 2000US-0747259.
R 28-FEB-2001; 2001US-0796498.
R 08-MAR-2001; 2001US-0802706.
R 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854290.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2003-332040/31.
DR N-PSDB; ACA03803.

XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in
PT tissue typing, and in chromosome identification -
XX
PS Claim 12; Fig 402; 660pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists
CC The PRO polypeptides are useful for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
CC the proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. ABU66570-ABU66844 represent the human
CC PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsIDentry.html.

XX Sequence 123 AA;

Query Match 100.0%; Score 123; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-117;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRCLSFLLMGTFELSVSQTVLALDALLVPPGVAQLSCITLSPQHVTIRDYGVSWYQQR 60
DB 1 MACRCLSFLLMGTFELSVSQTVLALDALLVPPGVAQLSCITLSPQHVTIRDYGVSWYQQR 60
QY 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAXDEAHNACVLITSPVQPEDDADYCSVGYG 120
DB 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAXDEAHNACVLITSPVQPEDDADYCSVGYG 120
QY 121 FSP 123
DB 121 FSP 123

RESULT 7
BU67046
D ABU67046 standard; Protein; 123 AA.
X C
X C ABU67046;
X T
X T 27-MAY-2003 (first entry)
X X
X X Human secreted/transmembrane, PRO, protein SEQ ID 402.
E X
X X Human; secreted protein; transmembrane protein; PRO;
W W inflammatory disease; organ failure; atherosclerosis; cardiac injury;
W W infertility; birth defects; premature aging; AIDS; biosensor;
W W acquired immunodeficiency syndrome; cancer; diabetic complication;
W W bioreactor; tumour.
X X
X X Homo sapiens.
X X
X X US2003032155-A1.
X X
X X 13-FEB-2003.
X X
X X 03-MAY-2002; 2002US-0137865.
X X
X X 31-MAR-1997; 97WO-US05230.
X X 12-JUN-1998; 98WO-US12456.
X X 14-JUL-1998; 98WO-US14552.
X X 28-AUG-1998; 98WO-US17888.
X X 10-SEP-1998; 98WO-US18924.
X X 14-SEP-1998; 98WO-US19093.
X X 14-SEP-1998; 98WO-US19094.
X X 14-SEP-1998; 98WO-US19177.
X X 16-SEP-1998; 98WO-US19330.
X X 17-SEP-1998; 98WO-US19437.
X X 07-OCT-1998; 98WO-US21141.
X X 29-OCT-1998; 98WO-US22991.
X X 29-OCT-1998; 98WO-US22992.
X X 20-NOV-1998; 98WO-US24855.
X X 01-DEC-1998; 98WO-US25108.
X X 05-JAN-1999; 99WO-US00106.
X X 08-MAR-1999; 99WO-US05028.
X X 10-MAR-1999; 99WO-US05190.
X X 20-APR-1999; 99WO-US08615.
X X 14-MAY-1999; 99WO-US10713.
X X 02-JUN-1999; 99WO-US12252.
X X 01-SEP-1999; 99WO-US20111.
X X 08-SEP-1999; 99WO-US20594.
X X 13-SEP-1999; 99WO-US20944.
X X 15-SEP-1999; 99WO-US21090.
X X 05-OCT-1999; 99WO-US21547.
X X 29-NOV-1999; 99WO-US23089.
X X 30-NOV-1999; 99WO-US28214.
X X 30-NOV-1999; 99WO-US28313.
X X 01-DEC-1999; 99WO-US28409.
X X 01-DEC-1999; 99WO-US28301.
X X 02-DEC-1999; 99WO-US28634.
X X 02-DEC-1999; 99WO-US28551.
X X 02-DEC-1999; 99WO-US28564.
X X 02-DEC-1999; 99WO-US28565.
X X 16-DEC-1999; 99WO-US30095.
X X 20-DEC-1999; 99WO-US30911.
X X 20-DEC-1999; 99WO-US30999.
X X 22-DEC-1999; 99WO-US30720.
X X 30-DEC-1999; 99WO-US31243.
X X 30-DEC-1999; 99WO-US31274.
X X 05-JAN-2000; 2000WO-US00219.
X X 06-JAN-2000; 2000WO-US00277.
X X 06-JAN-2000; 2000WO-US00376.
X X 11-FEB-2000; 2000WO-US03565.
X X 18-FEB-2000; 2000WO-US04341.
X X 18-FEB-2000; 2000WO-US04342.
X X 22-FEB-2000; 2000WO-US04414.
X X 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0805689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0865034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
PA (GETH) GENENTECH INC.
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-331925/31.
XX N-PSDB; ACA04224.
XX New secreted and transmembrane nucleic acids and polypeptides,
XX designated as PRO, useful for treating inflammation, organ failure,
XX atherosclerosis, cardiac injury, infertility, birth defects, premature
XX aging, AIDS, or cancer
XX Claim 12; Fig 402; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
XX at least 80% identical to, or the full-length coding sequence of, any of
XX the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
XX (one of 275 secreted or transmembrane proteins). The nucleic acid
XX further comprises the full-length coding sequence of the DNA deposited
XX under American Type Culture Collection (ATCC) accession number in a list

C given in the specification. Also included are vectors and host
C cells for producing PRO proteins, PRO fusion proteins, anti-PRO
C antibodies, PRO extracellular domains and mature sequences, methods
C of detecting PRO proteins, methods for stimulating the release of
C TNF-alpha (tumour necrosis factor alpha) from human blood,
C (and the proliferation of differentiation of chondrocyte cells, the
C proliferation of, or gene expression in pericyte cells, the release or
C proteoglycans from cartilage, proliferation of inner ear utricular
C supporting cells, the proliferation of T-lymphocyte cells, the release
C of a cytokine from peripheral blood mononuclear cells (PBMC), or the
C proliferation of endothelial cells), a method for modulating the uptake
C of glucose or free fatty acid (FFA) by skeletal muscle cells,
C a method for inhibiting the binding of A-peptide to factor VIIa,
C or the differentiation of adipocyte cells, a method for detecting the
C presence of a tumour in a mammal and an oligonucleotide probe derived
C from any of the nucleotide sequences cited above. The nucleic acids and
C polypeptides are useful for treating inflammatory diseases, organ
C failure, atherosclerosis, cardiac injury, infertility, birth defects,
C premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
C diabetic complications. The nucleic acids are useful as hybridisation
C probes, in chromosome and gene mapping, and in generating antisense RNA
C or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
C biosensors or bioreactors. Both are useful in tissue typing.
C The present sequence represents a PRO protein of the invention.

Q Sequence 123 AA;

Query Match 100.0%; Score 123; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-117;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MACRCLSFLIMGTFILSVSTVLAQLDALLVFPQVQLSCTLSPOHVTIRYGVSWYQQR 60
b 1 MACRCLSFLIMGTFILSVSTVLAQLDALLVFPQVQLSCTLSPOHVTIRYGVSWYQQR 60

Y 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDAAHNAACVLTISVPQEDDADYTCVGVYG 120
b 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDAAHNAACVLTISVPQEDDADYTCVGVYG 120

Y 121 FSP 123

b 121 FSP 123

RESULT 8

BU59851

D ABU59851 standard; Protein; 123 AA.

X ASU59851;

X 13-MAY-2003 (first entry)

X Novel secreted and transmembrane protein PRO619.

X Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
X cardiac insufficiency disorder; cancer; tumour; immune response;
X adrenal cortical capillary endothelial growth; c-fos induction;
X vascular endothelial growth factor inhibition; VEGF inhibition;
X endothelial cell growth inhibitor; T-lymphocytes stimulation;
X retinal neurons cell survival; rod photoreceptor cell survival;
X retinal disorder; retinitis pigmentosa; kidney disorder;
X mammalian kidney mesangial cell proliferation; Berger disease;
X dermatitis; hepatifomias; Crohn's disease; chondrocyte proliferation;
X chondrocyte redifferentiation; sports injury; arthritis.

X Homo sapiens.

X US2003017563-A1.

X 23-JAN-2003.

X 07-MAY-2002; 2002US-0140808.

PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 16-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 29-OCT-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 98WO-US25106.
PR 08-MAR-1999; 98WO-US25028.
PR 10-MAR-1999; 98WO-US25190.
PR 20-APR-1999; 98WO-US250615.
PR 14-MAY-1999; 98WO-US10733.
PR 02-JUN-1999; 98WO-US12252.
PR 01-SEP-1999; 98WO-US20111.
PR 08-SEP-1999; 98WO-US20594.
PR 13-SEP-1999; 98WO-US20944.
PR 15-SEP-1999; 98WO-US21090.
PR 15-SEP-1999; 98WO-US21547.
PR 05-OCT-1999; 98WO-US23089.
PR 23-NOV-1999; 98WO-US28214.
PR 30-NOV-1999; 98WO-US28313.
PR 30-NOV-1999; 98WO-US28409.
PR 01-DEC-1999; 98WO-US28301.
PR 01-DEC-1999; 98WO-US28634.
PR 02-DEC-1999; 98WO-US28551.
PR 02-DEC-1999; 98WO-US28564.
PR 02-DEC-1999; 98WO-US28565.
PR 16-DEC-1999; 98WO-US30095.
PR 20-DEC-1999; 98WO-US30911.
PR 20-DEC-1999; 98WO-US30999.
PR 22-DEC-1999; 98WO-US30720.
PR 30-DEC-1999; 98WO-US31243.
PR 30-DEC-1999; 98WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.

R 01-JUN-2001; 2001WO-US17800.
 R 20-JUN-2001; 2001WO-US19692.
 R 22-JUN-2001; 2001WO-US20116.
 R 29-JUN-2001; 2001WO-US21066.
 R 09-JUL-2001; 2001WO-US21735.
 R 28-DEC-2000; 2000US-0747259.
 R 28-FEB-2001; 2001US-0796498.
 R 09-MAR-2001; 2001US-0802706.
 R 14-MAR-2001; 2001US-0805689.
 R 22-MAR-2001; 2001US-0816744.
 R 05-APR-2001; 2001US-0828366.
 R 10-MAY-2001; 2001US-0854208.
 R 10-MAY-2001; 2001US-0854280.
 R 18-MAY-2001; 2001US-0860216.
 R 25-MAY-2001; 2001US-0866028.
 R 23-MAY-2001; 2001US-0866034.
 R 01-JUN-2001; 2001US-0872035.
 R 05-JUN-2001; 2001US-0874503.
 R 14-JUN-2001; 2001US-0882636.
 R 19-JUN-2001; 2001US-0886342.
 R 21-JUN-2001; 2001US-0887879.
 R 18-JUL-2001; 2001US-0908827.
 R 06-AUG-2001; 2001US-0924419.
 R 09-AUG-2001; 2001US-0927796.
 R 16-AUG-2001; 2001US-0931836.
 R 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Bersini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
 Grietsen ME, Goddard A, Godowski PV, Gurney AL, Sherwood S,
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
 WPI; 2003-148238/14.
 N-PSDB; ABX9341.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 are therapeutically useful for enhancing immune response and in cancer
 treatments -

Claim 12; Fig 402; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO
 polypeptides are useful in detecting PRO polypeptides in a sample, in
 linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 in modulating at least one biological activity of a cell expressing a PRO
 polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 stimulate adrenal cortical capillary endothelial growth, and PRO536,
 PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 useful for treating conditions or disorders where angiogenesis would be
 beneficial, e.g. wound healing and antagonist of this polypeptide are
 useful for treating cancerous tumours. PRO812 inhibits vascular
 endothelial growth factor (VEGF) stimulated proliferation of endothelial
 cells and is thus useful for inhibiting endothelial cell growth in
 mammals which would be beneficial in inhibiting tumour growth. PRO826,
 PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 stimulated T-lymphocytes and are therapeutically useful for enhancing
 immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
 retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 rod photoreceptor cells) and therefore are useful for treating retinal
 disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 and PRO11066 induce proliferation of mammalian kidney mesangial cells,
 and therefore are useful for treating kidney disorders associated with
 decreased mesangial cell function such as Berger disease or other
 nephropathies associated with dermatitis, herpeticiformis or Crohn's
 disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 proliferation and/or redifferentiation of chondrocytes in culture and
 are thus useful for treating sports injuries, and arthritis. This
 is the amino acid sequence of a novel human PRO protein.

SQ Sequence 123 AA;

Query Match 100.0%; Score 123; DB 24; Length 123;
 Best Local Similarity 100.0%; Pred. NO. 4.8e-117;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MACRCLSPFLMGTLFSLVSQTVLAQLDALLVFPQVAGLSCTLSFQHVITRDYGVSWYQQR 60
 QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDZAHNAACVLTISFQPEDDADYCSVGYG 120
 DB 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDZAHNAACVLTISFQPEDDADYCSVGYG 120
 QY 121 FSP 123
 DB 121 FSP 123

RESULT 9

ABUS9071

ID ABUS9071 standard; Protein; 123 AA.

XX AC ABUS9071;

XX DT 28-APR-2003 (first entry)

XX DE Novel human secreted or transmembrane protein PRO619.

XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;

XX KW cardiac insufficiency disorder; cancer; tumour; immune response;

XX KW adrenal cortical capillary endothelial growth; c-fos induction;

XX KW vascular endothelial growth factor inhibition; VEGF inhibition;

XX KW endothelial cell growth inhibitor; T-lymphocytes stimulation;

XX KW retinal neurons cell survival; rod photoreceptor cell survival;

XX KW retinal disorder; retinitis pigmentosa; kidney disease;

XX KW mammalian kidney mesangial cell proliferation; Berger disease;

XX KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;

XX KW chondrocyte redifferentiation; sports injury; arthritis.

XX OS Homo sapiens.

XX PN US2002132252-A1.

XX PD 19-SEP-2002.

XX PF 14-NOV-2001; 2001US-0990442.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US21108.

XX PR 06-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 01-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 01-DEC-1999; 99WO-US28634.

XX PR 18-DEC-1999; 99WO-US30095.

XX PR 20-DEC-1999; 99WO-US30911.

XX PR 06-JAN-2000; 2000WO-US00219.

XX PR 06-JAN-2000; 2000WO-US00376.

XX PR 11-FEB-2000; 2000WO-US03565.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 22-FEB-2000; 2000WO-US04414.

XX PR 24-FEB-2000; 2000WO-US04914.

XX PR 24-FEB-2000; 2000WO-US05004.

XX PR 02-MAR-2000; 2000WO-US05841.

XX PR 10-MAR-2000; 2000WO-US06319.

XX PR 15-MAR-2000; 2000WO-US06884.

R 20-MAR-2000; 2000WC-US07377.
R 30-MAR-2000; 2000WC-US08439.
R 15-MAY-2000; 2000WC-US13358.
R 17-MAY-2000; 2000WC-US13705.
R 22-MAY-2000; 2000WC-US14042.
R 30-MAY-2000; 2000WC-US14941.
R 02-JUN-2000; 2000WC-US15264.
R 28-JUL-2000; 2000WC-US20710.
R 11-AUG-2000; 2000WC-US22031.
R 23-AUG-2000; 2000WC-US23522.
R 08-NOV-2000; 2000WC-US23328.
R 01-DEC-2000; 2000WC-US32678.
R 28-FEB-2001; 2001WC-US06520.
R 01-JUN-2001; 2001WC-US17800.
R 20-JUN-2001; 2001WC-US19692.
R 29-JUN-2001; 2001WC-US21066.
R 09-JUL-2001; 2001WC-US21735.
R 16-JUN-1997; 97US-049787P.
R 17-OCT-1997; 97US-062250P.
R 12-NOV-1997; 97US-065186P.
R 13-NOV-1997; 97US-065311P.
R 24-NOV-1997; 97US-066770P.
R 25-FEB-1998; 98US-075945P.
R 20-MAR-1998; 98US-078910P.
R 28-APR-1998; 98US-083322P.
R 07-MAY-1998; 98US-084600P.
R 28-MAY-1998; 98US-087106P.
R 02-JUN-1998; 98US-087607P.
R 02-JUN-1998; 98US-087809P.
R 02-JUN-1998; 98US-087859P.
R 03-JUN-1998; 98US-088272P.
R 04-JUN-1998; 98US-088221P.
R 04-JUN-1998; 98US-088025P.
R 04-JUN-1998; 98US-088026P.
R 04-JUN-1998; 98US-088028P.
R 04-JUN-1998; 98US-088029P.
R 04-JUN-1998; 98US-088030P.
R 04-JUN-1998; 98US-088033P.
R 04-JUN-1998; 98US-088326P.
R 05-JUN-1998; 98US-088167P.
R 05-JUN-1998; 98US-088202P.
R 05-JUN-1998; 98US-088212P.
R 05-JUN-1998; 98US-088217P.
R 09-JUN-1998; 98US-088655P.
R 10-JUN-1998; 98US-088734P.
R 10-JUN-1998; 98US-088738P.
R 10-JUN-1998; 98US-088742P.
R 10-JUN-1998; 98US-088810P.
R 10-JUN-1998; 98US-088824P.
R 10-JUN-1998; 98US-088826P.
R 11-JUN-1998; 98US-088858P.
R 11-JUN-1998; 98US-088861P.
R 11-JUN-1998; 98US-088876P.
R 12-JUN-1998; 98US-089105P.
R 16-JUN-1998; 98US-089440P.
R 16-JUN-1998; 98US-089512P.
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R 17-JUN-1998; 98US-089600P.
R 18-JUN-1998; 98US-089653P.
R 18-JUN-1998; 98US-089801P.
R 18-JUN-1998; 98US-089807P.
R 18-JUN-1998; 98US-089908P.
R 28-AUG-2001; 2001US-0941992.

(GETH) GENENTECH INC.

A Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
I Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
DR WPI; 2003-247083/24.
DR N-PSDB; ABX80196.
XX
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX
XX
PS Claim 12; Fig 68; 648pp; English.
XX
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC is the amino acid sequence of a novel human PRO protein.
XX
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 123; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-117;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MACRLSFLMGTFSLVSQTVLAQLDALLYPPQVACLCTLSFQHTIRDYGVSYQQR 60
Db 1 MACRLSFLMGTFSLVSQTVLAQLDALLYPPQVACLCTLSFQHTIRDYGVSYQQR 60
QY 61 AGSAPRYLLYYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYYCVGYG 120
Db 61 AGSAPRYLLYYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYYCVGYG 120
QY 121 FSP 123
Db 121 FSP 123

RESULT 10

ABUS9218

ID ABUS9218 standard; Protein; 123 AA.

XX AC ABUS9218;
XX DT 22-APR-2003 (first entry)

XX Human secreted/transmembrane protein, #43.

W Human; PRO; secreted; transmembrane; pharmaceutical;
W diagnostic; biosensor; bioreactor; tumour; therapeutic;
W gene therapy; tumour-associated antigenic target; TAG; ADEPT;
W antibody-dependent enzyme mediated prodrug therapy; cytostatic.

IS Homo sapiens.

X US2003027162-A1.

N 06-FEB-2003.

D 15-NOV-2001; 2001US-0997428.

P 05-NOV-1997; 97WO-US20069.

X 16-SEP-1998; 98WO-US19330.

R 17-SEP-1998; 98WO-US19437.

R 07-OCT-1998; 98WO-US21141.

R 01-DEC-1998; 98WO-US25108.

R 05-JAN-1999; 99WO-US00106.

R 08-MAR-1999; 99WO-US05028.

R 02-JUN-1999; 99WO-US12252.

R 15-SEP-1999; 99WO-US21090.

R 15-SEP-1999; 99WO-US211547.

R 30-NOV-1999; 99WO-US28313.

R 01-DEC-1999; 99WO-US28301.

R 01-DEC-1999; 99WO-US28334.

R 16-DEC-1999; 99WO-US30095.

R 20-DEC-1999; 99WO-US30911.

R 05-JAN-2000; 2000WO-US00219.

R 06-JAN-2000; 2000WO-US00376.

R 11-FEB-2000; 2000WO-US03565.

R 18-FEB-2000; 2000WO-US04341.

R 22-FEB-2000; 2000WO-US04414.

R 24-FEB-2000; 2000WO-US04914.

R 24-FEB-2000; 2000WO-US05004.

R 02-MAR-2000; 2000WO-US05841.

R 10-MAR-2000; 2000WO-US06319.

R 15-MAR-2000; 2000WO-US06684.

R 20-MAR-2000; 2000WO-US07377.

R 30-MAR-2000; 2000WO-US08439.

R 15-MAY-2000; 2000WO-US13358.

R 17-MAY-2000; 2000WO-US13705.

R 22-MAY-2000; 2000WO-US14042.

R 30-MAY-2000; 2000WO-US14941.

R 02-JUN-2000; 2000WO-US15264.

R 28-JUL-2000; 2000WO-US20710.

R 11-AUG-2000; 2000WO-US22031.

R 23-AUG-2000; 2000WO-US23522.

R 24-AUG-2000; 2000WO-US23328.

R 08-NOV-2000; 2000WO-US30952.

R 01-DEC-2000; 2000WO-US32678.

R 28-FEB-2001; 2001WO-US06520.

PR 04-JUN-1998; 98US-088028P.
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PR 23-JUN-1998; 98US-090355P.
PR 23-JUN-1998; 98US-090429P.
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PR 26-JUN-1998; 98US-090862P.
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PR 01-JUL-1998; 98US-091360P.
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PR 02-JUL-1998; 98US-091646P.
PR 02-JUL-1998; 98US-091673P.
PR 07-JUL-1998; 98US-091978P.
PR 07-JUL-1998; 98US-091982P.
PR 09-JUL-1998; 98US-092182P.
PR 10-JUL-1998; 98US-092472P.
PR 20-JUL-1998; 98US-093339P.
PR 30-JUL-1998; 98US-094651P.

R 04-AUG-1998; 98US-095282P.
R 04-AUG-1998; 98US-095285P.
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R 04-AUG-1998; 98US-095318P.
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R 04-AUG-1998; 98US-096143P.
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R 04-AUG-1998; 98US-096959P.
R 04-AUG-1998; 98US-096960P.
R 04-AUG-1998; 98US-097022P.
R 04-AUG-1998; 98US-097141P.
R 04-AUG-1998; 98US-097218P.
R 04-AUG-1998; 98US-097661P.
R 04-AUG-1998; 98US-097952P.
R 04-AUG-1998; 98US-097954P.
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R 04-AUG-1998; 98US-097978P.
R 04-AUG-1998; 98US-097979P.
R 04-AUG-1998; 98US-097986P.
R 04-AUG-1998; 98US-098014P.
R 04-AUG-1998; 98US-098525P.
R 04-AUG-1998; 98US-100634P.
R 04-SEP-1998; 98US-100634P.
R 04-SEP-1998; 98US-100858P.
R 04-DEC-1998; 98US-113296P.
R 04-DEC-1998; 98US-113296P.
R 04-DEC-1998; 98US-123957P.
R 04-JUN-1999; 98US-141037P.

Query Match 100.0%; Score 123; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-117;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MACRLSFLMGTFLVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSMYQQR 60
b 1 MACRLSFLMGTFLVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSMYQQR 60

Y 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLITSPVQPEDDADYYCVGYG 120
b 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLITSPVQPEDDADYYCVGYG 120

Y 121 FSP 123
b 121 FSP 123

RESULT 11
BU59367
D ABUS9367 standard; Protein; 123 AA.
X
C ABUS9367;
X
I 22-APR-2003 (first entry)
X
E Novel human secreted or transmembrane protein PRO943.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adiac cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX Homo sapiens.
OS US2003027985-A1.
XX 06-FEB-2003.
PD 14-NOV-2001; 2001US-0990562.
PF 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
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PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
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PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062500P.
PR 12-NOV-1997; 97US-065186P.
PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.

R 02-JUN-1998; 98US-087607P.
R 02-JUN-1998; 98US-087609P.
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R 03-JUN-1998; 98US-087827P.
R 04-JUN-1998; 98US-088021P.
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R 04-JUN-1998; 98US-088026P.
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R 10-JUN-1998; 98US-088810P.
R 10-JUN-1998; 98US-088824P.
R 10-JUN-1998; 98US-088826P.
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R 12-JUN-1998; 98US-089440P.
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PR 26-AUG-1998; 98US-097978P.
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PR 26-AUG-1998; 98US-098014P.

Query Match 100.0%; Score 123; DB 24; Length 123;

Best Local Similarity 100.0%; Pred. No. 4.8e-117; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVQVLAQLSCTLSPOHVTIRDYGVSWYQQR 60
DB 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVQVLAQLSCTLSPOHVTIRDYGVSWYQQR 60
QY 61 AGSAPRYLLYRSEDEHRRPADIPDRFSAKDEAHNAACVLTISPQPEDDADYYCSVGYG 120
DB 61 AGSAPRYLLYRSEDEHRRPADIPDRFSAKDEAHNAACVLTISPQPEDDADYYCSVGYG 120

QY 121 FSP 123

DB 121 FSP 123

RESULT 12

ABU60502

ID ABU60502 standard; Protein; 123 AA.

XX ABU60502;

AC ABU60502;

XX 01-MAY-2003 (first entry)

DT

XX


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Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2y 1 MACCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
db 1 MACCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
2y 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYCSVGYG 120
db 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYCSVGYG 120
2y 121 FSP 123
db 121 FSP 123

RESULT 13
ABUS7993
ID ABUS7993 standard; Protein; 123 AA.
AC ABUS7993;
JT 14-APR-2003 (first entry)
DE Human PRO polypeptide #25.
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
KS Homo sapiens.
KN US2003027163-A1.
PD 06-FEB-2003.
PF 15-NOV-2001; 2001US-0997666.
PR 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
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PR 30-NOV-1999; 99WO-US28313.
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PR 05-JAN-2000; 2000WO-US00219.
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PR 11-FEB-2000; 2000WO-US03565.
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PR 28-JUL-2000; 2000WO-US20710.
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R 26-JUN-1998; 98US-090862P.
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Best Local Similarity 100.0%; Pred. No. 4.8e-117;
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QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISFVQPEDDADYCVSYGYG 120
DB 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISFVQPEDDADYCVSYGYG 120
QY 121 FSP 123
DB 121 FSP 123

RESULT 14
ABUS8924
ID ABUS8924 standard; Protein; 123 AA.
XX
AC ABUS8924;
XX
DT 16-APR-2003 (first entry)
DE Human secreted/transmembrane protein, #43.
XX
KW Human; PRO; secreted; transmembrane; signal peptide;
KW Pharmaceutical; diagnostic; biosensor; bioindicator; tumour; therapeutic;
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002142961-A1.
XX
PD 03-OCT-2002.
XX
PF 19-NOV-2001; 2001US-0989721.
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PR 05-NOV-1997; 97WO-US20069.
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PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
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PR 30-MAR-2000; 2000WO-US08439.
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PR 30-MAY-2000; 2000WO-US14941.
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PR 28-JUL-2000; 2000WO-US20710.
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XX	01-DEC-2000;	200WO-US32678.	
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CC	01-JUN-2001;	200WO-US17800.	
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CC	12-OCT-1997;	97US-062250P.	
CC	12-NOV-1997;	97US-065196P.	
CC	13-NOV-1997;	97US-065311P.	
CC	24-NOV-1997;	97US-066770P.	
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CC	28-MAR-1998;	98US-078910P.	
CC	28-APR-1998;	98US-083332P.	
CC	07-MAY-1998;	98US-084600P.	
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CC	02-JUN-1998;	98US-087759P.	
CC	03-JUN-1998;	98US-087827P.	
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CC	10-JUN-1998;	98US-088824P.	
CC	10-JUN-1998;	98US-088826P.	
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CC	12-JUN-1998;	98US-089105P.	
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CC	16-JUN-1998;	98US-089512P.	
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XX	(GETH) GENENTECH INC.		
XX	Ashtenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
PI	Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;		
PI	Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;		
PI	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;		
PI	Zhang Z;		
XX	WPI; 2003-155950/15.		
DR	New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,		
PT	PRO361 or PRO946) useful as targets for therapeutic intervention in		
PT	cancers (e.g. lung or breast cancers), or for diagnosing these cancers		
PT			
XX			

Claim 12; Fig 68; 647pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits, as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention.

Sequence 123 AA;

Query Match	100.0%;	Score 123;	DB 24;	Length 123;
Best Local Similarity	100.0%;	Pred. No. 4.8e-117;		
Matches 123;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MACRCCLFLLMGTFELSVSGTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGSWYQQR 60

DB 1 MACRCCLFLLMGTFELSVSGTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGSWYQQR 60

QY 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYCSVGYG 120

DB 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYCSVGYG 120

QY 121 FSP 123

DB 121 FSP 123

RESULT 15

ABU13884

ID ABU13884 standard; Protein; 123 AA.

XX AC ABU13884;

XX DT 26-FEB-2003 (first entry)

XX DE Human PRO619 polypeptide.

XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;

XX KW genetic disorder; antibacterial; immunosuppressive.

XX OS Homo sapiens.

XX PN US2002103125-A1.

XX PD 01-AUG-2002.

XX PF 20-NOV-2001; 200IUS-0989731.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 01-DEC-1999; 99WO-US28634.

R 16-DEC-1999; 99WO-US30095.
R 20-DEC-1999; 99WO-US30911.
R 06-JAN-2000; 2000WO-US00219.
R 06-JAN-2000; 2000WO-US00376.
R 11-FEB-2000; 2000WO-US03565.
R 18-FEB-2000; 2000WO-US04341.
R 22-FEB-2000; 2000WO-US04414.
R 24-FEB-2000; 2000WO-US04914.
R 02-MAR-2000; 2000WO-US05004.
R 10-MAR-2000; 2000WO-US05941.
R 15-MAR-2000; 2000WO-US06319.
R 20-MAR-2000; 2000WO-US06884.
R 30-MAR-2000; 2000WO-US07377.
R 15-MAY-2000; 2000WO-US08439.
R 17-MAY-2000; 2000WO-US13358.
R 22-MAY-2000; 2000WO-US13705.
R 30-MAY-2000; 2000WO-US14042.
R 02-JUN-2000; 2000WO-US14941.
R 08-JUN-2000; 2000WO-US15264.
R 28-JUL-2000; 2000WO-US20710.
R 11-AUG-2000; 2000WO-US22031.
R 23-AUG-2000; 2000WO-US23522.
R 24-AUG-2000; 2000WO-US23328.
R 08-NOV-2000; 2000WO-US30952.
R 01-DEC-2000; 2000WO-US32678.
R 28-FEB-2001; 2001WO-US06520.
R 01-JUN-2001; 2001WO-US17800.
R 20-JUN-2001; 2001WO-US19692.
R 29-JUN-2001; 2001WO-US21066.
R 09-JUL-2001; 2001WO-US21735.
R 16-JUN-1997; 97US-049787P.
R 17-OCT-1997; 97US-062250P.
R 12-NOV-1997; 97US-065186P.
R 13-NOV-1997; 97US-065311P.
R 24-NOV-1997; 97US-066770P.
R 25-FEB-1998; 98US-075945P.
R 20-MAR-1998; 98US-078910P.
R 28-APR-1998; 98US-083322P.
R 07-MAY-1998; 98US-084600P.
R 28-MAY-1998; 98US-087106P.
R 02-JUN-1998; 98US-087607P.
R 02-JUN-1998; 98US-087609P.
R 02-JUN-1998; 98US-087759P.
R 03-JUN-1998; 98US-087827P.
R 04-JUN-1998; 98US-088021P.
R 04-JUN-1998; 98US-088025P.
R 04-JUN-1998; 98US-088026P.
R 04-JUN-1998; 98US-088028P.
R 04-JUN-1998; 98US-088029P.
R 04-JUN-1998; 98US-088030P.
R 04-JUN-1998; 98US-088033P.
R 05-JUN-1998; 98US-088326P.
R 05-JUN-1998; 98US-088167P.
R 05-JUN-1998; 98US-088202P.
R 05-JUN-1998; 98US-088212P.
R 05-JUN-1998; 98US-088217P.
R 09-JUN-1998; 98US-088655P.
R 10-JUN-1998; 98US-088734P.
R 10-JUN-1998; 98US-088739P.
R 10-JUN-1998; 98US-088742P.
R 10-JUN-1998; 98US-088810P.
R 10-JUN-1998; 98US-088824P.
R 10-JUN-1998; 98US-088826P.
R 11-JUN-1998; 98US-088858P.
R 11-JUN-1998; 98US-088861P.
R 12-JUN-1998; 98US-088876P.
R 12-JUN-1998; 98US-089105P.
R 16-JUN-1998; 98US-089440P.
R 16-JUN-1998; 98US-089512P.
R 16-JUN-1998; 98US-089514P.
R 17-JUN-1998; 98US-089532P.
R 17-JUN-1998; 98US-089538P.
R 17-JUN-1998; 98US-089598P.

PR 17-JUN-1998; 98US-089599P.
PR 17-JUN-1998; 98US-089600P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089801P.
PR 18-JUN-1998; 98US-089907P.
PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-0941992.
PA (GETH) GENENTECH LTD.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen WE, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI: 2003-102117/09.
DR N-PSDB; ABX64020.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers -
XX
PS Claim 12; Fig 68; 649pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, to construct
CC hybridisation probes for mapping the gene which encodes the PRO
CC polypeptide, and for the genetic analysis of individuals with genetic
CC disorders, in gene therapy, for generating probes for PCR, Northern
CC chromosome markers, and for generating probes for PCR, Northern
CC analysis, Southern analysis and Western analysis. ABU13860-ABU14006
CC represent the human PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsbIDentry.html.
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 123; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-117;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MACRCLSFLMGTFILSVQTVLAQLDALLVFPFGVAQLSCTLSPOHVTIRDYGVSWYQQR 60
Db 1 MACRCLSFLMGTFILSVQTVLAQLDALLVFPFGVAQLSCTLSPOHVTIRDYGVSWYQQR 60

Qy 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQVEDDADYCSGVYG 120
Db 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQVEDDADYCSGVYG 120

Qy 121 FSP 123
Db 121 FSP 123

RESULT 16
ABU10839
ID ABU10839 standard; Protein; 123 AA.
XX
AC ABU10839;
XX
DT 04-FEB-2003 (first entry)
XX

DE Human PRO polypeptide #25.
CX Human; PRO: secreted polypeptide; transmembrane polypeptide;
CX toxin; radiolabel; cell death; gene mapping; chromosome mapping;
CX protein electrophoresis; Genetic disorder; immunosuppressive; cytostatic;
CX antibacterial.
CX Homo sapiens.
CX US2002123463-A1.
CX 05-SEP-2002.
CX 19-NOV-2001; 2001US-0969732.
CX 05-NOV-1997; 97WO-US20069.
CX 16-SEP-1998; 98WO-US19330.
CX 17-SEP-1998; 98WO-US19437.
CX 07-OCT-1998; 98WO-US21141.
CX 01-DEC-1998; 98WO-US25108.
CX 05-JAN-1999; 99WO-US00106.
CX 08-MAR-1999; 99WO-US05028.
CX 02-JUN-1999; 99WO-US12252.
CX 15-SEP-1999; 99WO-US21090.
CX 30-NOV-1999; 99WO-US21547.
CX 01-DEC-1999; 99WO-US28313.
CX 01-DEC-1999; 99WO-US28301.
CX 01-DEC-1999; 99WO-US28634.
CX 16-DEC-1999; 99WO-US30095.
CX 20-DEC-1999; 99WO-US30911.
CX 06-JAN-2000; 2000WO-US00219.
CX 06-JAN-2000; 2000WO-US00376.
CX 11-FEB-2000; 2000WO-US03565.
CX 18-FEB-2000; 2000WO-US04341.
CX 22-FEB-2000; 2000WO-US04414.
CX 24-FEB-2000; 2000WO-US04914.
CX 24-FEB-2000; 2000WO-US05004.
CX 02-MAR-2000; 2000WO-US05841.
CX 10-MAR-2000; 2000WO-US06319.
CX 15-MAR-2000; 2000WO-US06894.
CX 20-MAR-2000; 2000WO-US07377.
CX 30-MAR-2000; 2000WO-US08439.
CX 15-MAY-2000; 2000WO-US13358.
CX 17-MAY-2000; 2000WO-US13705.
CX 22-MAY-2000; 2000WO-US14042.
CX 30-MAY-2000; 2000WO-US14941.
CX 02-JUN-2000; 2000WO-US15264.
CX 28-JUL-2000; 2000WO-US20710.
CX 11-AUG-2000; 2000WO-US22031.
CX 23-AUG-2000; 2000WO-US23522.
CX 24-AUG-2000; 2000WO-US23328.
CX 08-NOV-2000; 2000WO-US30952.
CX 01-DEC-2000; 2000WO-US32678.
CX 28-FEB-2001; 2001WO-US06520.
CX 01-JUN-2001; 2001WO-US17800.
CX 20-JUN-2001; 2001WO-US19692.
CX 29-JUN-2001; 2001WO-US21066.
CX 09-JUL-2001; 2001WO-US21735.
CX 16-JUN-1997; 97US-049787P.
CX 17-OCT-1997; 97US-062250P.
CX 12-NOV-1997; 97US-065186P.
CX 13-NOV-1997; 97US-065311P.
CX 24-NOV-1997; 97US-066770P.
CX 25-FEB-1998; 98US-075945P.
CX 20-MAR-1998; 98US-078910P.
CX 28-APR-1998; 98US-083322P.
CX 28-MAY-1998; 98US-084600P.
CX 02-JUN-1998; 98US-087106P.
CX 02-JUN-1998; 98US-087609P.
CX 02-JUN-1998; 98US-087759P.
CX 03-JUN-1998; 98US-087827P.
CX 04-JUN-1998; 98US-088021P.

PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088026P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088030P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088734P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088742P.
PR 10-JUN-1998; 98US-088810P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088858P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089440P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089532P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089599P.
PR 17-JUN-1998; 98US-089600P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089801P.
PR 18-JUN-1998; 98US-089907P.
PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-0941992.
XX (GETH) GENENTECH INC.
FA Atkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferraz N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2003-066810/06.
DR N-PSDB; ABX16984.
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers -
PS Claim 12; Fig 68; 655pp; English.

The invention relates to a secreted and transmembrane polypeptide, termed PRO polypeptide, and the polynucleotide encoding it. The polypeptide is useful for detecting PRO polypeptides and for linking a bioactive molecule to a cell expressing the above polypeptides, where the bioactive molecule is a toxin, radiolabel or an antibody. The bioactive material causes the death of the cell. The polypeptide is useful for identifying agonists or antagonists of the PRO polypeptide, for preparing variants of PRO, as a molecular weight marker for protein electrophoresis purposes and the PRO polynucleotide is also useful for recombinantly expressing those markers. The polynucleotide is also useful as a hybridisation probe, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation probes for mapping the gene which encodes PRO and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as a chromosome marker and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. This sequence represents a human PRO polypeptide of the invention.

CC Sequence 123 AA;
 Query Match 100.0%; Score 123; DB 24; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4.8e-117;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MACRCFLMGTFLLSVQVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
 b 1 MACRCFLMGTFLLSVQVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60
 Y 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYYCSVGYG 120
 b 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYYCSVGYG 120
 Y 121 FSP 123
 b 121 FSP 123

RESULT 17
 IAM39690
 ID AAM39690 standard; Protein; 141 AA.
 CC AAM39690;
 CC
 CC
 CC 22-OCT-2001 (first entry)
 CC Human polypeptide SEQ ID NO 2835.
 CC Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
 CC peripheral nervous system; neuropathy; central nervous system; CNS;
 CC Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 CC amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 CC chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 CC leukaemia.
 CC
 CC Homo sapiens.
 CC WO200153312-A1.
 CC 26-JUL-2001.
 CC 26-DEC-2000; 2000WO-US34263.
 CC 21-JAN-2000; 2000US-0488725.
 CC 25-APR-2000; 2000US-0552317.
 CC 09-JUL-2000; 2000US-0598042.
 CC 19-JUL-2000; 2000US-0620312.
 CC 03-AUG-2000; 2000US-0653450.
 CC 14-SEP-2000; 2000US-0682191.
 CC 19-OCT-2000; 2000US-0693036.
 CC 29-NOV-2000; 2000US-0727344.
 CC (HYSEQ-) HYSEQ INC.
 CC Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 CC Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 CC Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 CC WPI; 2001-442253/47.
 CC N-PSDB; AAI58846.
 CC Novel nucleic acids and polypeptides, useful for treating disorders
 CC such as central nervous system injuries -
 CC Example 4; SEQ ID NO 2835; 10078pp; English.
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nontropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 CC Sequence 141 AA;
 Query Match 96.7%; Score 119; DB 22; Length 141;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLMGTFLLSVQVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSA 64
 b 23 CLSFLMGTFLLSVQVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSA 82
 QY 65 PRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYYCSVGFGSP 123
 b 83 PRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYYCSVGFGSP 141

RESULT 18
 AAM41476
 ID AAM41476 standard; Protein; 113 AA.
 CC AAM41476;
 CC 22-OCT-2001 (first entry)
 CC Human polypeptide SEQ ID NO 6407.
 CC Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
 CC peripheral nervous system; neuropathy; central nervous system; CNS;
 CC Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 CC amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 CC chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 CC leukaemia.
 CC
 CC Homo sapiens.
 CC WO200153312-A1.
 CC 26-JUL-2001.
 CC 26-DEC-2000; 2000WO-US34263.
 CC 21-JAN-2000; 2000US-0488725.
 CC 25-APR-2000; 2000US-0552317.
 CC 09-JUL-2000; 2000US-0598042.
 CC 19-JUL-2000; 2000US-0620312.
 CC 03-AUG-2000; 2000US-0653450.
 CC 14-SEP-2000; 2000US-0662191.
 CC 19-OCT-2000; 2000US-0693036.
 CC 29-NOV-2000; 2000US-0727344.
 CC (HYSEQ-) HYSEQ INC.
 CC Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 CC Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 CC Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 CC WPI; 2001-442253/47.
 CC N-PSDB; AAI60632.
 CC Novel nucleic acids and polypeptides, useful for treating disorders
 CC such as central nervous system injuries -
 CC

PS Example 2; SEQ ID NO 6407; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AA386642-AA42213) with neurotropic,
XX immunosuppressant and cytostatic activity. The polypeptide or polynucleotide
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.

XX Sequence 113 AA;

Query Match 87.0%; Score 107; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 8.2e-101;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VSCQTLAQDALLVFPQGVQAOISCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEED 76

Db 7 VSCQTLAQDALLVFPQGVQAOISCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEED 66

QY 77 HRRPADIPRFSAAKDEAHNACVLTISVPQEDDADYYCVSVGYGFSP 123

Db 67 HRRPADIPRFSAAKDEAHNACVLTISVPQEDDADYYCVSVGYGFSP 113

RESULT 19

ABP45354

ID ABP45354 standard; Protein; 258 AA.

XX AC ABP45354;

DT 19-AUG-2002 (first entry)

DE Human BlyS binding scFv SEQ ID 1365.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

XX 17-OCT-2000; 2000US-240816P.

XX 16-MAR-2001; 2001US-276248P.

XX 21-MAR-2001; 2001US-277379P.

XX 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for

the diagnosis and treatment of cancers and immune disorders -

PS Claim 1; Page 2031-2032; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be
XX administered to treat diseases associated with aberrant BlyS expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.

XX Sequence 258 AA;

Query Match 7.3%; Score 9; DB 23; Length 258;

Best Local Similarity 100.0%; Pred. No. 0.76;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 EDDADYYCS 116

Db 230 EDDADYYCS 238

RESULT 20

AA38953

ID AA38953 standard; Protein; 235 AA.

XX AC AA38953;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2098.

XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0582317.

XX 09-JUL-2000; 2000US-0596042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;

WPI; 2001-442253/47.
N-PSDB; AA158109.
Novel nucleic acids and polypeptides, useful for treating disorders
such as central nervous system injuries -
Example 3; SEQ ID NO 2098; 10078pp; English.
The invention relates to human nucleic acids (AA157798-AA161369) and
the encoded polypeptides (AA157798-AA161369) with neurotrophic,
immunomodulatory and cytoskeletal activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral neuropathies, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilization of the activities such as: immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
specification.

Sequence 235 AA;
Query Match 6.5%; Score 8; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

108 EDDADYYC 115
99 EDDADYYC 106
|||||

RESULT 21
AAE20273
AAE20273 standard; Protein; 246 AA.
AAE20273;
18-JUN-2002 (first entry)
Human lung specific gene (LSG) protein #11.
Human; lung specific gene; LSG; lung embryonic development; cytostatic;
lung cancer; vaccine; Gene therapy; non-cancerous lung disease; tumour.
Homo sapiens.
Key Location/Qualifiers
Region 189..204
/note= "Antigenic epitope"
WO200208278-A2.
31-JAN-2002.
20-JUL-2001; 2001WO-US22949.
21-JUL-2000; 2000US-219834P.
(DIAD-) DIADEXUS INC.
Macina RA, Nair M, Chen S;
WPI; 2002-268964/31.
Novel lung specific gene useful for identifying, diagnosing,
monitoring, staging, imaging and treating lung cancer and non-cancerous
disease states in lung, for gene therapy, and for identifying lung
tissue -

Claim 2; Page 178-179; 197pp; English.
The present invention relates to lung specific genes (LSG) and their
corresponding polypeptides. LSG is useful for identifying, diagnosing,
monitoring, staging, imaging and treating lung cancer and non-cancerous
disease states in lung, identifying lung tissue, monitoring and
modifying lung embryonic development and differentiation, in gene
therapy, as hybridisation probes, to detect LSG mRNA as a marker for
lung cancer, as research reagents and materials for discovery of
treatments and diagnostics to human disease, to detect complementary
polynucleotides, and for chromosome identification. An antibody which
binds LSG is useful to detect or image localisation of LSG in a patient
for detecting or diagnosing a disease or condition, for preventing the
onset and treatment of lung cancer, to isolate or to identify clones
expressing LSG polypeptides, to purify LSG polypeptides, and to target
tumours expressing LSG. The present sequence is human LSG protein.

Sequence 246 AA;
Query Match 6.5%; Score 8; DB 23; Length 246;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

81 ADIPDRFS 88
80 ADIPDRFS 87
|||||

RESULT 22
ABG66690
ID ABG66690 standard; Protein; 526 AA.
AC ABG66690;
30-AUG-2002 (first entry)
Human novel polypeptide #25.
Human; inflammatory condition; shock; sepsis; immune response;
cancer; wound healing; central nervous system disease; haematopoiesis;
peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
bone degenerative disorder; periodontal disease; reperfusion injury;
lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
allergic condition; thrombolysis; thrombosis; coagulation disorder;
fungal infection.
Homo sapiens.
WO200244340-A2.
06-JUN-2002.
30-NOV-2001; 2001WO-US47004.
30-NOV-2000; 2000US-0028952.
(HYSE-) HYSEQ INC.
Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
Yamazaki V, Ujwal ML, Drmanac RT;
WPI; 2002-508509/54.
N-PSDB; ABK94914.
Novel nucleic acids and polypeptides for diagnosis, treatment of
inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
disorders, cancer and promoting wound healing -
Claim 10; Page 591-592; 672pp; English.

CC The invention relates to human novel polynucleotides and associated
 CC polypeptides. The polynucleotides and polypeptides are useful for
 CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
 CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
 CC and cancer and for promoting wound healing. The sequences are used to
 CC induce the proliferation of neural cells and regeneration of nerve and
 CC brain tissue, and are useful for the treatment of central and peripheral
 CC nervous system diseases and neuropathies, such as Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease and amyotrophic lateral
 CC sclerosis. The sequences are involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
 CC cell disorders and platelet disorders such as thrombocytopenia,
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
 CC disease. The sequences of the invention are also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC including severe combined immunodeficiency (SCID), bacterial or fungal
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
 CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic
 CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human
 CC novel polypeptides of the invention.

XX Sequence 526 AA;
 SQ

Query Match 6.5%; Score 8; DB 23; Length 526;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108
 DB 96 TISPVQPE 103
 |||||

RESULT 23
 ABG66689
 ID ABG66689 standard; Protein; 588 AA.

AC ABG66689;

XX 30-AUG-2002 (first entry)

DE Human novel polypeptide #24.

XX Human; inflammatory condition; shock; sepsis; immune response;
 KW cancer; wound healing; central nervous system disease; haematopoiesis;
 KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
 KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
 KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
 KW bone degenerative disorder; periodontal disease; reperfusion injury;
 KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
 KW allergic condition; thrombolytic; thrombosis; coagulation disorder;
 KW fungal infection.

XX Homo sapiens.

XX WO200244340-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-US47004.

XX 30-NOV-2000; 2000US-0028952.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;

PI Yamazaki V, Ujwal ML, Dmanac RT;

XX WPI; 2002-508509/54.

DR N-PSDB; ABK94913.

XX

PT Novel nucleic acids and polypeptides for diagnosis, treatment of
 PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
 PT disorders, cancer and promoting wound healing -
 XX Claim 10; Page 590-591; 672pp; English.
 XX
 CC The invention relates to human novel polynucleotides and associated
 CC polypeptides. The polynucleotides and polypeptides are useful for
 CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
 CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
 CC and cancer and for promoting wound healing. The sequences are used to
 CC induce the proliferation of neural cells and regeneration of nerve and
 CC brain tissue, and are useful for the treatment of central and peripheral
 CC nervous system diseases and neuropathies, such as Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease and amyotrophic lateral
 CC sclerosis. The sequences are involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
 CC cell disorders and platelet disorders such as thrombocytopenia, and
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
 CC disease. The sequences of the invention are also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC including severe combined immunodeficiency (SCID), bacterial or fungal
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
 CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic
 CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human
 CC novel polypeptides of the invention.

SQ Sequence 588 AA;

Query Match 6.5%; Score 8; DB 23; Length 588;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108
 DB 96 TISPVQPE 103
 |||||

RESULT 24

AAE01020

ID AAE01020 standard; Protein; 689 AA.

XX AAE01020;

XX 17-JUL-2001 (first entry)

DT Human pif-1 type helicase protein.

DE Human; pif-1 type helicase; cytostatic; antiinflammatory; antiviral;
 XX antisense therapy; telomerase; cellular senescence; cancer; tumour;
 KW lymphoma; leukaemia; viral replication disease; retroviral disease.

XX Homo sapiens.

XX WO200130986-A2.

XX 03-MAY-2001.

XX 18-OCT-2000; 2000WO-US28780.

XX 22-OCT-1999; 99US-0425335.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Weinmann R, Yang W;

XX WPI; 2001-300502/31.

DR N-PSDB; AAD04757.

XX Novel human homolog of yeast helicase, Pif-1 useful for generating

T antibodies for detection of hPif1 protein for diagnostic or clinical
 T purposes, and for screening drugs which either modulate helicase
 T activity

Claim 9; Fig 2; 57pp; English.

X The present protein sequence is human homologue of yeast
 X helicase, Pif-1. Pif-1 type helicase affects the formation of
 X elongation of telomerase and/or interaction with components of
 X the replication machinery. They are also involved in Arp binding
 X or hydrolysis. Pif-1 modulators are useful for modulating a disorder
 X which are characterised by the presence of cells exhibiting elevated
 X helicase activity or decreased telomerase activity, or vice versa.
 X Pif-1 or Pif-1 modulators are used to treat cellular senescence,
 X cancer, tumours (e.g. solid tumours, lymphomas, leukaemia), viral
 X replication diseases (including DNA and RNA viral replication diseases
 X such as retroviral diseases and herpes) and inflammatory responses.
 X Pif-1 is useful for generating antibodies for detection of human
 X Pif-1 (hPif-1) protein for diagnostic or clinical purposes, and for
 X screening drugs which either increase or decrease the activity of
 X Pif-1. Pif-1 DNA is useful in antisense therapy.

Sequence 689 AA;

Query Match 6.5%; Score 8; DB 22; Length 689;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

101 TISPVQPE 108

149 TISPVQPE 156

RESULT 25

ABG21666

ID ABG21666 standard; Protein; 1249 AA.

AC ABG21666;

18-FEB-2002 (first entry)

Novel human diagnostic protein #21657.

Human; chromosome mapping; gene mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Drmanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

N-PGDB; AAS85853.

New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 biodiversity

Claim 20; SEQ ID No 52025; 103pp; English.

The invention relates to isolated polynucleotide (I) and

polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1249 AA;

Query Match 6.5%; Score 8; DB 22; Length 1249;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 RCLSFLLM 11

1037 RCLSFLLM 1044

RESULT 26

ABP76447

ID ABP76447 standard; Peptide; 14 AA.

AC ABP76447;

24-FEB-2003 (first entry)

Peptidomimetic antimicrobial peptide related peptide SEQ ID NO:79.

Template-fixed peptidomimetic; antimicrobial; beta-hairpin; cytostatic;
 antibacterial; infection; cystic fibrosis; lung infection; malignant;
 cancer; disinfectant; preservative.

Synthetic.

WO200270547-A1.

12-SEP-2002.

18-FEB-2002; 2002WO-EP01711.

23-FEB-2001; 2001WO-EP02072.

(POLY-) POLYPHOS LTD.

(UVZU-) UNIV ZUERICH.

Obrecht D, Robinson JA, Vrijbloed JW;

WPI; 2003-103173/09.

New beta-hairpin peptidomimetic compounds, useful for treating
 infections, especially cystic fibrosis lung infections and cancer, and
 as disinfectants/preservatives for e.g. foodstuffs or cosmetics -

Example; Page 159; 262pp; English.

The present invention describes template-fixed beta-hairpin
 CC peptidomimetic compounds (I) and (II). Also described: (1) preparation
 CC of (I) and (II); and (2) a modification of the preparation in which
 CC enantiomers or all chiral starting materials are used. (I) and (II) have
 CC antibacterial and cytostatic activities. The peptidomimetic compounds

CC are useful for treating or preventing infections or diseases related to
 CC such infections, especially cystic fibrosis lung infections; for
 CC preparing medicaments useful against malignant cells for treatment of
 CC cancer; as disinfectants or preservatives for foodstuffs, cosmetics,
 CC medicaments and other nutrient-containing materials; and for preventing
 CC microbial colonisation of surfaces. ABP76369 to ABP76677 represent
 CC peptide sequences used in the exemplification of the present invention.

XX Sequence 14 AA;

Query Match 5.7%; Score 7; DB 24; Length 14;

Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 RYLLYYR 72

DB 8 RYLLYYR 14

RESULT 27

ABP76448

ID ABP76448 standard; Peptide; 14 AA.

XX ABP76448;

XX 24-FEB-2003 (first entry)

XX Peptidomimetic antimicrobial peptide related peptide SEQ ID NO:80.

XX Template-fixed peptidomimetic; antimicrobial; beta-hairpin; cytostatic;
 KW antibacterial; infection; cystic fibrosis; lung infection; malignant;
 KW cancer; disinfectant; preservative.

XX Synthetic.

XX WO200270547-A1.

XX 12-SEP-2002.

XX 18-FEB-2002; 2002WO-EP01711.

XX 23-FEB-2001; 2001WO-EP02072.

XX (POLY-) POLYPHOS LTD.

XX (UYZU-) UNIV ZUERICH.

XX Obrecht D, Robinson JA, Vrijbloed JW;

XX WPI; 2003-103173/09.

XX New beta-hairpin peptidomimetic compounds, useful for treating
 PT infections, especially cystic fibrosis lung infections and cancer, and
 PT as disinfectants/preservatives for e.g. foodstuffs or cosmetics -

XX Example; Page 159; 262pp; English.

XX The present invention describes template-fixed beta-hairpin
 CC peptidomimetic compounds (I) and (II). Also described: (i) preparation
 CC of (I) and (II); and (2) a modification of the preparation in which
 CC enantiomers or all chiral starting materials are used. (I) and (II) have
 CC antibacterial and cytostatic activities. The peptidomimetic compounds
 CC are useful for treating or preventing infections or diseases related to
 CC such infections, especially cystic fibrosis lung infections; for
 CC preparing medicaments useful against malignant cells for treatment of
 CC cancer; as disinfectants or preservatives for foodstuffs, cosmetics,
 CC medicaments and other nutrient-containing materials; and for preventing
 CC microbial colonisation of surfaces. ABP76369 to ABP76677 represent
 CC peptide sequences used in the exemplification of the present invention.

XX Sequence 14 AA;

Query Match

Best Local Similarity 5.7%; Score 7; DB 24; Length 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 RYLLYYR 72

DB 8 RYLLYYR 14

RESULT 28

AAR80091
 ID AAR80091 standard; Protein; 103 AA.

XX AAR80091;

XX 23-MAY-1996 (first entry)

XX Human derived light chain RT3 phage antibody.

XX Light chain; RT3; human; catalytic antibody; bacteriophage.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..16

XX /note= "framework region 1"

XX Region 17..27

XX /note= "complementarity determining region 1"

XX Region 28..43

XX /note= "framework region 2"

XX Region 44..49

XX /note= "complementarity determining region 2"

XX Region 50..82

XX /note= "framework region 3"

XX Region 83..92

XX /note= "complementarity determining region 3"

XX Region 93..103

XX /note= "framework region 4"

XX WO9527045-A1.

XX 12-OCT-1995.

XX 30-MAR-1994; 94WO-US03420.

XX 30-MAR-1994; 94WO-US03420.

XX (IGEN-) IGEN INC.

XX Chiswell D, Daraley MJ, Fitzgerald K, Kenten JH;

XX Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;

XX WPI; 1995-358624/46.

XX N-PSDB; AAT04638.

XX Production of catalytic antibodies displayed on phage - by
 PT generating a gene library of antibody-derived domains and expressing
 PT it in phage vectors

XX Disclosure; Fig 20; 133pp; English.

XX AAT04638 encodes AAR80091 human derived light chain RT3 phage antibody.
 CC The DNA was used in the prepn. of catalytic antibody (CA) producing
 CC bacteriophage. The CA can be used to activate/deactivate a
 CC biological function in an animal by enhancing the rate of cleavage,
 CC or formation of a specific bond within a mol. in vivo.

XX Sequence 103 AA;

Query Match

Best Local Similarity 5.7%; Score 7; DB 16; Length 103;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 IPDRFSA 89

```
Db 51 IPDRFSA 57
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 29
AAW95489
ID AAW95489 standard; Protein; 103 AA.
AC AAW95489;
XX
XX
XX 29-MAR-1999 (first entry)
XX
XX Human-derived RT3 phage antibody light chain genetic sequence.
XX
XX Catalytic; antibody; phage display; immunising; phage expression vector;
XX prodrug; scfv; RT3.
XX
XX Homo sapiens.
XX
XX US5855885-A.
XX
XX 05-JAN-1999.
XX
XX 14-JUL-1994; 94US-0273146.
XX
XX 22-JAN-1993; 93US-0007684.
XX
XX 14-JUL-1994; 94US-0273146.
XX
XX (CHIS/) CHISWELL D.
XX (DARS/) DARSLEY M J.
XX (FITZ/) FITZGERALD K.
XX (KENT/) KENTEN J H.
XX (MART/) MARTIN M T.
XX (MCCA/) MCCAFFERTY J.
XX (SMIT/) SMITH R.
XX (TITM/) TITMAS R C.
XX (WILL/) WILLIAMS R O.
XX
XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
XX Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
XX WPI: 1999-105036/09.
XX N-PSDB; AAX00888.
XX
XX Production of catalytic antibodies displayed on bacteriophages -
XX comprises generating a gene library of antibody-derived domains
XX inserting coding into a phage expression vector and isolating the
XX catalytic antibodies
XX
XX Examples; Fig 20F; 117pp; English.
XX
XX The invention relates to methods for producing catalytic antibodies
XX displayed on a phage. The method comprises: (a) generating a gene
XX library of antibody-derived domains; (b) inserting coding for the domains
XX into a phage expression vector; and (c) isolating the catalytic
XX antibodies. The phage expression vector incorporates a histidine peptide
XX in tandem with a myc peptide. The catalytic antibodies can be isolated by
XX preparing an antigen; optionally immunising an animal with the antigen;
XX generating a library of VH and VL domains from the immunised animal;
XX cloning the VH and VL domains into a phage expression vector to generate
XX phage display antibodies; selecting phage display antibodies which bind
XX specifically to the antigen; screening the selected phage display
XX antibodies for catalytic activity to substrate; and isolating the
XX catalytic antibodies, where the phage expression vector incorporates a
XX histidine peptide in tandem with a myc peptide. The processes are used to
XX produce catalytic antibodies, which can be used for in vivo activation of
XX a prodrug. Sequences AAW95484-489 represent genetic sequences of heavy
XX and light chains of RT3 specific phage antibodies selected from a naive
XX human phage antibody library.
XX
XX Sequence 103 AA;
XX
XX Query Match 5.7%; Score 7; DB 20; Length 103;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 IPDRFSA 89
Db 51 IPDRFSA 57
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 30
AAR26962
ID AAR26962 standard; Protein; 104 AA.
AC AAR26962;
XX
XX 25-MAR-2003 (updated)
XX 11-FEB-1993 (first entry)
XX
XX Human T lymphocyte receptor V-beta w23 subfamily segment.
XX
XX TCR; IGR b 04; variable region; immunomodulation;
XX polymerase chain reaction; T cell receptor.
XX
XX Homo sapiens.
XX
XX WO9213950-A2.
XX
XX 20-AUG-1992.
XX
XX 12-FEB-1992; 92WO-FR00130.
XX
XX 12-FEB-1991; 91FR-0001613.
XX 12-APR-1991; 91FR-0004523.
XX
XX (ROUS) ROUSSEL-UCLAF.
XX
XX Ferradini L, Hercend T, Roman-Roman S, Triebel F;
XX WPI: 1992-300036/36.
XX N-PSDB; AAQ28175.
XX
XX Variable regions of b-chain of T-lymphocyte receptors and their
XX DNA - useful as immuno:modulant(s) and for diagnosing immune
XX disorders
XX
XX Claim 7; Page 39; 75pp; French.
XX
XX RNA was isolated from peripheral lymphocytes and converted to cDNA
XX using a C-beta-specific primer. The cDNA was amplified by anchored
XX PCR using C-beta and polyC primers, then amplified again using a
XX different C-beta specific primer. The amplified product was SacII-
XX restricted, inserted into Bluescript SK+ vector and used to transform
XX E.coli XL-1blue. Transformants were screened with a C-beta specific
XX probe and DNA from positive clones was sequenced in the C-beta
XX region. The sequence designated "IGR b 04" is a consensus sequence
XX from 4 distinct cDNA clones. The sequence has an homology of 75.7%
XX with the sequence Vb12A1 (see Leiden J.M., et al., Proc. Natl. Acad.
XX Sci. USA, 83:4456, 1986) but has a homology of less than 75% with
XX other members of the Vbeta 5 subfamily. IGR b 04 is, therefore, not
XX a member of the Vbeta 5 subfamily. The peptide encoded by it can be
XX used to block T cell epitopes and in vaccines.
XX See also AAQ28173-Q28228.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 104 AA;
XX
XX Query Match 5.7%; Score 7; DB 13; Length 104;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 IPDRFSA 89
Db 70 IPDRFSA 76
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 31
AAR54313
ID AAR54313 standard; protein; 104 AA.
XX AC AAR54313;
XX DT 25-MAR-2003 (updated)
XX DT 10-NOV-1994 (first entry)
XX DE Anti-HIV gp120 immunoglobulin light chain variable region s3.
XX KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
XX KW neutralisation; monoclonal antibody; kappa light chain;
XX KW variable region; framework; complementarity determining region.
XX OS Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX FT Region 1..18
XX FT /label= FR1
XX FT Region 19..30
XX FT /label= CDR1
XX FT Region 31..45
XX FT /label= FR2
XX FT Region 46..52
XX FT /label= CDR2
XX FT Region 53..84
XX FT /label= FR3
XX FT Region 85..93
XX FT /label= CDR3
XX FT Region 94..104
XX FT /label= FR4
XX PN WO9407922-A1.
XX PD 14-APR-1994.
XX PF 30-SEP-1993; 93WO-US09328.
XX PF 30-SEP-1992; 92US-0954148.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Burton DR, Lerner RA;
XX WI WPI; 1994-135516/16.
XX DR New human monoclonal antibodies neutralising HIV - react with
XX PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
XX PT or in vitro diagnosis and for passive immuno-therapy
XX PS Example; Page 181-182; 248pp; English.
XX CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
XX CC amplification using primers specific for heavy and light chain
XX CC variable regions. The amplification products were inserted into a
XX CC dicistronic vector to produce a library of fragments. E.coli XL1
XX CC Blue cells were transformed with the library. Filamentous phage were
XX CC produced which expressed the MAb regions on their surface. Panning
XX CC with gp120 and gp41 resulted in the recovery of immunoreactive
XX CC clones. The light chain VK region sequence AAR54313 is from a gp120-
XX CC specific clone.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 104 AA;
```

```
Query Match 5.7%; Score 7; DB 15; Length 104;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 DIPDRFS 88
DB 53 DIPDRFS 59
```

```
RESULT 32
AAW01271
ID AAW01271 standard; Protein; 104 AA.
XX AC AAW01271;
XX DT 28-JAN-1997 (first entry)
XX DE VL region of HIV neutralising MAb, clone s3.
XX KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
XX KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
XX KW virus infectivity assay; precursor gp160; immunocompetence; human;
XX KW anti-HIV antibody; detection; HIV infection.
XX OS Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX FT Region 1..18
XX FT /label= FR1
XX FT Region 19..30
XX FT /label= CDR1
XX FT Region 31..45
XX FT /label= FR2
XX FT Region 46..52
XX FT /label= CDR2
XX FT Region 53..84
XX FT /label= FR3
XX FT Region 85..93
XX FT /label= CDR3
XX FT Region 94..104
XX FT /label= FR4
XX PN WO9602273-A1.
XX PD 01-FEB-1996.
XX PF 11-JUL-1995; 95WO-US08743.
XX PF 18-JUL-1994; 94US-0276852.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Burton DR, Lerner RA;
XX WI WPI; 1996-178601/18.
XX DR Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
XX PT passive immuno-therapy and detection of HIV infection.
XX PS Example; Fig 11; 366pp; English.
XX CC The sequences given in AAW01261-92 represent the light chain variable
XX CC regions (VL) of a series of monoclonal antibodies (MAbs) which are
XX CC immunoreactive with HIV glycoprotein gp120 and are capable of
XX CC neutralising HIV. This sequence represents the sequence of the JK2
XX CC gene clone, s3. A MAb containing this VL sequence has the capacity
XX CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
XX CC by 50 % at a concentration of less than 700 ng of antibody/ml. and
XX CC binds mature gp120 preferentially over the precursor gp160. The MAb
XX CC may be used for determining immunocompetence of a human anti-HIV
XX CC antibody and in the detection of HIV infection.
XX SQ Sequence 104 AA;
```

```
Query Match 5.7%; Score 7; DB 17; Length 104;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 DIPDRFS 88
DB 53 DIPDRFS 59
```

jb 53 DIPDRFS 59

RESULT 33
AY95123
D AAY95123 standard; Protein; 104 AA.

AC AAY95123;
AT 30-JUN-2000 (first entry)
DE Anti-gp120 antibody light chain variable region from clone s3.
KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

OS Homo sapiens.
XX AU9948756-A.
XX 17-FEB-2000.
XX 16-SEP-1999; 99AU-0048756.
XX 16-SEP-1999; 99AU-0048756.
XX (SCRI) SCRIPPS RES INST.
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 2000-293393/26.
XX Novel human monoclonal antibodies which immunoreact with and neutralise
XX human immunodeficiency virus useful for treating HIV infections -
XX Example 9; Figure 11; 366pp; English.

XX The present sequence represents a fragment of an anti-human
XX immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
XX a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
XX mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
XX gp160 and neutralises HIV and which reduces HIV infectivity titre in an
XX in vitro virus infectivity assay by 50%, at a concentration of less than
XX 700 ng/ml. The antibodies are used as reagents for the diagnosis and
XX immunotherapy of HIV induced disease. They are useful as neutralising
XX field isolates and provide useful information regarding the
XX immunocompetence of an immune response in HIV infected patients. The
XX monoclonal antibodies are useful for producing anti-idiotypic antibodies
XX which can be used to screen human monoclonal antibodies to identify
XX whether the antibody has the same binding specificity as the antibodies
XX of the invention. The neutralising antibodies define new epitopes on the
XX HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
XX immunotherapeutic human monoclonal antibodies. A major advantage of the
XX monoclonal antibodies derives from the fact that they are encoded by a
XX human polynucleotide sequence. Thus in vivo use of the monoclonal
XX antibodies for diagnosis and immunotherapy of HIV induced disease greatly
XX reduces the problems of significant host immune response to the passively
XX administered antibodies which is a problem commonly encountered when
XX monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
XX An additional major advantage of the monoclonal antibodies described
XX derives from the fact that they immunoreact with a unique determinant
XX present on mature HIV glycoprotein gp120. This class of antibodies is
XX particularly effective at neutralising field isolates of HIV.

XX Sequence 104 AA;
XX Query Match 5.7%; Score 7; DB 21; Length 104;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 82 DIPDRFS 88
|||||

Db 53 DIPDRFS 59

RESULT 34
AY98232
D AAY98232 standard; Protein; 104 AA.

AC AAY98232;
AT 04-JUL-2000 (first entry)
DE Anti-gp120 antibody light chain variable region from clone s3.
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.

OS Homo sapiens.
XX AU9948754-A.
XX 17-FEB-2000.
XX 16-SEP-1999; 99AU-0048754.
XX 16-SEP-1999; 99AU-0048754.
XX (SCRI) SCRIPPS RES INST.
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 2000-246867/22.
XX Human neutralising monoclonal antibodies to human immunodeficiency
XX virus (HIV) used for providing passive immunotherapy to HIV are
XX specific for glycoprotein-120 -
XX Example 9; Figure 11; 374pp; English.

XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
XX capable of reducing an HIV infectivity titre in an in vitro virus
XX infectivity assay by 50% at a concentration of less than 70 ng/ml. The
XX method for the production of the antibody comprises:
XX (a) providing a first polynucleotide encoding a heavy chain
XX immunoglobulin amino acid sequence (which does not comprise the sequence
XX represented by AAY98206) and a second polynucleotide encoding a light
XX chain immunoglobulin amino acid sequence;
XX (b) inserting the first and second polynucleotide sequences into a host
XX cell;
XX (c) maintaining the host cell in conditions which allow the amino acid
XX sequences encoded by the polynucleotides to be expressed in the host
XX cell; and
XX (d) isolating the antibody comprising the heavy and light chain
XX immunoglobulin amino acid sequences from the host cell.
XX The anti-HIV gp-120 monoclonal antibody is used for providing passive
XX immunotherapy to HIV in a human. They can be administered to high-risk
XX patients to reduce the likelihood and/or severity of HIV-induced disease
XX and to patients who are already HIV-infected. The antibodies are used
XX for neutralising field isolates which provides information about the
XX immunocompetence of an immune response in HIV patients, for detecting
XX HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX producing anti-idiotypic antibodies which can be used for active
XX immunisation and to screen human monoclonal antibodies to identify those
XX with the same binding specificity and to monitor the course of HIV
XX disease therapy by measuring the changes in concentration of HIV present
XX in the body or in body fluids by immunoassay. The anti-HIV gp-120
XX monoclonal antibodies are encoded by a human polynucleotide sequence and
XX when used in vivo for diagnosis and immunotherapy of HIV-induced disease
XX reduce the problems of significant host immune response to the
XX antibodies associated with monoclonal antibodies of xenogeneic or

CC chimeric derivation.

SQ Sequence 104 AA;

Query Match 5.7%; Score 7; DB 21; Length 104;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88

Db 53 DIPDRFS 59

RESULT 35

ABG22849

ID ABG22849 standard; Protein; 105 AA.

XX AC ABG22849;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #22840.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Dmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS87036.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity

XX PS Claim 20; SEQ ID No 53208; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

XX CC polynucleotides are also used in diagnostics as expressed sequence tags

XX CC for identifying expressed genes. (I) is useful in gene therapy techniques

XX CC to restore normal activity of (II) or to treat disease states involving

XX CC (II). (II) is useful for generating antibodies against it, detecting or

XX CC quantitating a polypeptide in tissue, as molecular weight markers and as

XX CC a food supplement. (II) and its binding partners are useful in medical

XX CC imaging of sites expressing (II). (I) and (II) are useful for treating

XX CC disorders involving aberrant protein expression or biological activity.

XX CC The polypeptide and polynucleotide sequences have applications in

XX CC diagnostics, forensics, gene mapping, identification of mutations

XX CC responsible for genetic disorders or other traits to assess biodiversity

XX CC and to produce other types of data and products dependent on DNA and

XX CC amino acid sequences. ABG00010-ABG30377 represent novel human

XX CC diagnostic amino acid sequences of the invention.

XX CC Note: The sequence data for this patent did not appear in the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 105 AA;

Query Match 5.7%; Score 7; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 PRYLLEY 71

Db 46 PRYLLEY 52

RESULT 36

AAR50217

ID AAR50217 standard; Protein; 109 AA.

XX AC AAR50217;

XX DT 25-MAR-2003 (updated)

XX DT 31-OCT-1994 (first entry)

XX DE HSV glycoprotein F binding MAB clone rsv6/11/21/22L VH/VL domain.

XX KW Complementarity determination region; CDR3; human; bronchiolitis;

XX KW monoclonal antibody; epitope; glycoprotein F; influenza virus;

XX KW respiratory syncytial virus; RSV; disease; rhinovirus; coronavirus;

XX KW lung; pneumonia.

XX OS Synthetic.

XX PH Key

XX FT Region 1..23

XX FT Region 24..35

XX FT Region 36..50

XX FT Region 51..57

XX FT Region 58..89

XX FT Region 90..98

XX FT Region 99..109

XX FT Region 1..109

XX FT Region 1..109

XX FT Region 1..109

XX FT Region 1..109

XX FT Region 1..109

XX FT Region 1..109

XX FT Region 1..109

XX FT Region 1..109

XX FT Region 1..109

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XX FT Region 1..109

XX FT Region 1..109

XX FT Region 1..109

CC may also be used for treating pneumonia and bronchiolitis.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 109 AA;

Query Match 5.7%; Score 7; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 82 DIPDRFS 88

2b 58 DIPDRFS 64

RESULT 37

AAB98230
ID AAB98230 standard; Protein; 109 AA.

AC AAB98230;

20-AUG-2001 (first entry)

Rabbit anti-A33 antigen antibody VL1 polypeptide SEQ ID NO:21.

Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
immunoglobulin; complementarity determining region; CDR; cancer;
cytostatic; anticancer; colon cancer; stomach cancer.

Oryctolagus cuniculus.

Homo sapiens.

WO200130393-A2.

03-MAY-2001.

20-OCT-2000; 2000WO-US29289.

22-OCT-1999; 99US-0425638.

04-APR-2000; 2000US-0543004.

(LUDW-) LUDWIG INST CANCER RES.

(SLOK) SLOAN KETTERING INST CANCER RES.

(SCRI) SCRIPPS RES INST.

Barbas CF, Rader C, Ritter G, Welt S, Old LJ;

WPI; 2001-328613/34.

Treating cancers, particularly of stomach and colon, that express A33
antigen by administering conjugate of anticancer agent with specific
immunoglobulin product.

Example 3; Fig 1; 85pp; English.

The present invention describes a method for treating cancers that
express the A33 antigen. The method comprises administering an
anticancer agent (I) conjugated to an immunoglobulin product (II) that
binds specifically to A33 and contains one or more of 13 specified
complementarity determining regions (CDRs), given in AAB98262 to
AAB98274. (I) has cytostatic activity. The method can be used for
treating colon and stomach cancers. (II), or the nucleic acid encoding
it, can be used directly, in unconjugated form, for immunotherapy of
cancer, and, when labeled, for detection or diagnosis of diseases
associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
AAB98321 represent sequences used in the exemplification of the
present invention.

SQ Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GVSWYQQ 59

Db 32 GVSWYQQ 38

RESULT 38

AAB98231
ID AAB98231 standard; Protein; 109 AA.

AC AAB98231;

20-AUG-2001 (first entry)

Rabbit anti-A33 antigen antibody VL2 polypeptide SEQ ID NO:22.

Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
immunoglobulin; complementarity determining region; CDR; cancer;
cytostatic; anticancer; colon cancer; stomach cancer.

Oryctolagus cuniculus.

Homo sapiens.

WO200130393-A2.

03-MAY-2001.

20-OCT-2000; 2000WO-US29289.

22-OCT-1999; 99US-0425638.

04-APR-2000; 2000US-0543004.

(LUDW-) LUDWIG INST CANCER RES.

(SLOK) SLOAN KETTERING INST CANCER RES.

(SCRI) SCRIPPS RES INST.

Barbas CF, Rader C, Ritter G, Welt S, Old LJ;

WPI; 2001-328613/34.

Treating cancers, particularly of stomach and colon, that express A33
antigen by administering conjugate of anticancer agent with specific
immunoglobulin product.

Example 3; Fig 1; 85pp; English.

The present invention describes a method for treating cancers that
express the A33 antigen. The method comprises administering an
anticancer agent (I) conjugated to an immunoglobulin product (II) that
binds specifically to A33 and contains one or more of 13 specified
complementarity determining regions (CDRs), given in AAB98262 to
AAB98274. (I) has cytostatic activity. The method can be used for
treating colon and stomach cancers. (II), or the nucleic acid encoding
it, can be used directly, in unconjugated form, for immunotherapy of
cancer, and, when labeled, for detection or diagnosis of diseases
associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
AAB98321 represent sequences used in the exemplification of the
present invention.

SQ Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GVSWYQQ 59

Db 32 GVSWYQQ 38

RESULT 39

AAB98232
ID AAB98232 standard; Protein; 109 AA.

XX

```
AC AAB98232;
XX
XX 20-AUG-2001 (first entry)
XX
XX Rabbit anti-A33 antigen antibody VLB polypeptide SEQ ID NO:23.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
XX immunoglobulin; complementarity determining region; CDR; cancer;
XX cytostatic; anticancer; colon cancer; stomach cancer.
XX
XX Oryctolagus cuniculus.
XX
XX Homo sapiens.
XX
XX WO200130393-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29289.
XX
XX 22-OCT-1999; 99US-0425638.
XX
XX 04-APR-2000; 2000US-0543004.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (SLOK) SLOAN KETTERING INST-CANCER RES.
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX
XX WPI; 2001-328613/34.
XX
XX Treating cancers, particularly of stomach and colon, that express A33
XX antigen by administering conjugate of anticancer agent with specific
XX immunoglobulin product -
XX
XX Example 3; Fig 1; 85pp; English.
XX
XX The present invention describes a method for treating cancers that
XX express the A33 antigen. The method comprises administering an
XX anticancer agent (I) conjugated to an immunoglobulin product (II) that
XX binds specifically to A33 and contains one or more of 13 specified
XX complementarity determining regions (CDRs), given in AAB98262 to
XX AAB98274. (I) has cytostatic activity. The method can be used for
XX treating colon and stomach cancers. (II), or the nucleic acid encoding
XX it, can be used directly, in unconjugated form, for immunotherapy of
XX cancer, and, when labeled, for detection or diagnosis of diseases
XX associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
XX AAB98321 represent sequences used in the exemplification of the
XX present invention.
XX
XX Sequence 109 AA;
XX
XX Query Match 5.7%; Score 7; DB 22; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 53 GVSWYQQ 59
XX |||||
XX 32 GVSWYQQ 38
XX
XX RESULT 40
XX AAB98233
XX ID AAB98233 standard; Protein; 109 AA.
XX
XX AC AAB98233;
XX
XX 20-AUG-2001 (first entry)
XX
XX Humanised anti-A33 antigen antibody VLA polypeptide SEQ ID NO:39.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
XX immunoglobulin; complementarity determining region; CDR; cancer;
XX cytostatic; anticancer; colon cancer; stomach cancer.
XX
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XX OS Homo sapiens.
XX
XX WO200130393-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29289.
XX
XX 22-OCT-1999; 99US-0425638.
XX
XX 04-APR-2000; 2000US-0543004.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX
XX WPI; 2001-328613/34.
XX
XX Treating cancers, particularly of stomach and colon, that express A33
XX antigen by administering conjugate of anticancer agent with specific
XX immunoglobulin product -
XX
XX Example 5; Fig 1; 85pp; English.
XX
XX The present invention describes a method for treating cancers that
XX express the A33 antigen. The method comprises administering an
XX anticancer agent (I) conjugated to an immunoglobulin product (II) that
XX binds specifically to A33 and contains one or more of 13 specified
XX complementarity determining regions (CDRs), given in AAB98262 to
XX AAB98274. (I) has cytostatic activity. The method can be used for
XX treating colon and stomach cancers. (II), or the nucleic acid encoding
XX it, can be used directly, in unconjugated form, for immunotherapy of
XX cancer, and, when labeled, for detection or diagnosis of diseases
XX associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
XX AAB98321 represent sequences used in the exemplification of the
XX present invention.
XX
XX Sequence 109 AA;
XX
XX Query Match 5.7%; Score 7; DB 22; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 53 GVSWYQQ 59
XX |||||
XX 32 GVSWYQQ 38
XX
XX RESULT 41
XX AAB98234
XX ID AAB98234 standard; Protein; 109 AA.
XX
XX AC AAB98234;
XX
XX 20-AUG-2001 (first entry)
XX
XX Humanised anti-A33 antigen antibody VLB polypeptide SEQ ID NO:40.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
XX immunoglobulin; complementarity determining region; CDR; cancer;
XX cytostatic; anticancer; colon cancer; stomach cancer.
XX
XX Homo sapiens.
XX
XX WO200130393-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29289.
XX
XX 22-OCT-1999; 99US-0425638.
XX
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CC complementarity determining regions (CDRs), given in AAB98262 to
CC AAB98274. (I) has cytotostatic activity. The method can be used for
CC treating colon and stomach cancers. (II), or the nucleic acid encoding
CC it, can be used directly, in unconjugated form, for immunotherapy of
CC cancer, and, when labeled, for detection or diagnosis of diseases
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
CC AAB98321 represent sequences used in the exemplification of the
CC present invention.

XX SQ Sequence 109 AA;
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSQYQQ 59
DB 32 GVSQYQQ 38

RESULT 44
AAB98237
ID AAB98237 standard; Protein; 109 AA.
XX AC AAB98237;
XX DT 20-AUG-2001 (first entry)
XX DE Humanised anti-A33 antigen antibody VLE polypeptide SEQ ID NO:43.
XX KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW immunoglobulin; complementarity determining region; CDR; cancer;
KW cytotostatic; anticancer; colon cancer; stomach cancer.
XX OS Homo sapiens.
XX PN WO200130393-A2.
XX PD 03-MAY-2001.
XX PF 20-OCT-2000; 2000WO-US29289.
XX PR 22-OCT-1999; 99US-0425638.
XX PR 04-APR-2000; 2000US-0543004.
XX PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (SCRI) SCRIPPS RES INST.
XX PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX WPI; 2001-328613/34.
XX DR Treating cancers, particularly of stomach and colon, that express A33
PT antigen by administering conjugate of anticancer agent with specific
PT immunoglobulin product -
XX Example 5; Fig 1; 85pp; English.
XX The present invention describes a method for treating cancers that
CC express the A33 antigen. The method comprises administering an
CC anticancer agent (I) conjugated to an immunoglobulin product (II) that
CC binds specifically to A33 and contains one or more of 13 specified
CC complementarity determining regions (CDRs), given in AAB98262 to
CC AAB98274. (I) has cytotostatic activity. The method can be used for
CC treating colon and stomach cancers. (II), or the nucleic acid encoding
CC it, can be used directly, in unconjugated form, for immunotherapy of
CC cancer, and, when labeled, for detection or diagnosis of diseases
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
CC AAB98321 represent sequences used in the exemplification of the
CC present invention.

XX SQ Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSQYQQ 59
DB 32 GVSQYQQ 38

RESULT 45
AAB98238
ID AAB98238 standard; Protein; 109 AA.
XX AC AAB98238;
XX DT 20-AUG-2001 (first entry)
XX DE Humanised anti-A33 antigen antibody VLF polypeptide SEQ ID NO:44.
XX KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW immunoglobulin; complementarity determining region; CDR; cancer;
KW cytotostatic; anticancer; colon cancer; stomach cancer.
XX OS Homo sapiens.
XX PN WO200130393-A2.
XX PD 03-MAY-2001.
XX PF 20-OCT-2000; 2000WO-US29289.
XX PR 22-OCT-1999; 99US-0425638.
XX PR 04-APR-2000; 2000US-0543004.
XX PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (SCRI) SCRIPPS RES INST.
XX PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX WPI; 2001-328613/34.
XX DR Treating cancers, particularly of stomach and colon, that express A33
PT antigen by administering conjugate of anticancer agent with specific
PT immunoglobulin product -
XX Example 5; Fig 1; 85pp; English.
XX The present invention describes a method for treating cancers that
CC express the A33 antigen. The method comprises administering an
CC anticancer agent (I) conjugated to an immunoglobulin product (II) that
CC binds specifically to A33 and contains one or more of 13 specified
CC complementarity determining regions (CDRs), given in AAB98262 to
CC AAB98274. (I) has cytotostatic activity. The method can be used for
CC treating colon and stomach cancers. (II), or the nucleic acid encoding
CC it, can be used directly, in unconjugated form, for immunotherapy of
CC cancer, and, when labeled, for detection or diagnosis of diseases
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
CC AAB98321 represent sequences used in the exemplification of the
CC present invention.

XX SQ Sequence 109 AA;
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSQYQQ 59
DB 32 GVSQYQQ 38

```

RESULT 46
AAB98239
ID AAB98239 standard; Protein; 109 AA.
XX
AC AAB98239;
XX
DT 20-AUG-2001 (first entry)
XX
DE Humanised anti-A33 antigen antibody VL polypeptide SEQ ID NO:45.
XX
KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW immunoglobulin; complementarity determining region; CDR; cancer;
KW cytostatic; anticancer; colon cancer; stomach cancer.
XX
OS Homo sapiens.
XX
PN WO200130393-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29289.
XX
PR 22-OCT-1999; 99US-0425638.
PR 04-APR-2000; 2000US-0543004.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C, Ritter G, Weit S, Old LJ;
XX
DR WPI; 2001-328613/34.
XX
PT Treating cancers, particularly of stomach and colon, that express A33
PT antigen by administering conjugate of anticancer agent with specific
PT immunoglobulin product
XX
PS Example 5; Fig 1; 85pp; English.
XX
CC The present invention describes a method for treating cancers that
CC express the A33 antigen. The method comprises administering an
CC anticancer agent (I) conjugated to an immunoglobulin product (II) that
CC binds specifically to A33 and contains one or more of 13 specified
CC complementarity determining regions (CDRs), given in AAB98262 to
CC AAB98274. (I) has cytostatic activity. The method can be used for
CC treating colon and stomach cancers. (II), or the nucleic acid encoding
CC it, can be used directly, in unconjugated form, for immunotherapy of
CC cancer, and, when labeled, for detection or diagnosis of diseases
CC associated with A33 expression. AAH2218 to AAH2254 and AAB98230 to
CC AAB98321 represent sequences used in the exemplification of the
CC present invention.
XX
SQ Sequence 109 AA;
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 GVSQYQQ 59
Db 32 GVSQYQQ 38
RESULT 47
AAB75149
ID AAB75149 standard; Protein; 109 AA.
XX
AC AAB75149;
XX
DT 08-AUG-2001 (first entry)
XX
DE Rabbit anti A33 antigen antibody V region VL1 SEQ ID NO:20.
XX
KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW immunoreact; anti A33 antigen antibody.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT Region 1..23 /label= FR1
FT Region 24..34 /label= CDR1
FT Region 35..49 /label= FR2
FT Region 50..56 /label= CDR2
FT Region 57..88 /label= FR3
FT Region 89..99 /label= CDR3
FT Region 100..109 /label= FR4
XX
PN WO200131065-A1.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29026.
XX
PR 22-OCT-1999; 99US-0425638.
PR 04-APR-2000; 2000US-0543004.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C;
XX
DR WPI; 2001-328657/34.
XX
PT Preparing humanized rabbit antibodies that specifically immunoreact
PT with a particular antigen using display technology for expressing
PT libraries of antibody domains and fine tuning variable domain regions -
XX
PS Example 4; Fig 1A; 62pp; English.
XX
CC The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarity determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human
CC mammalian antibodies, which can be used for the treatment of a variety
CC of diseases. The present sequence represents a rabbit anti A33 antigen
CC antibody V region protein sequence which is given in an example from the
CC present invention.
XX
SQ Sequence 109 AA;
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 GVSQYQQ 59
Db 32 GVSQYQQ 38
RESULT 48
AAB75150
ID AAB75150 standard; Protein; 109 AA.
XX
AC AAB75150;
XX
DT 08-AUG-2001 (first entry)
XX

```

DE Rabbit anti A33 antigen antibody V region VL2 SEQ ID NO:21.
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW immunoreact; anti A33 antigen antibody.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..34
FT /label= CDR1
FT Region 35..49
FT /label= FR2
FT Region 50..56
FT /label= CDR2
FT Region 57..88
FT /label= FR3
FT Region 89..99
FT /label= CDR3
FT Region 100..109
FT /label= FR4
XX WO200131065-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29026.
XX
XX 22-OCT-1999; 99US-0425638.
XX 04-APR-2000; 2000US-0543004.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX WPI; 2001-328657/34.
XX
XX Preparing humanized rabbit antibodies that specifically immunoreact
PT with a particular antigen using display technology for expressing
PT libraries of antibody domains and fine tuning variable domain regions -
XX
XX Example 4; Fig 1A; 62pp; English.
XX
XX The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarity determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human
CC mammalian antibodies, which can be used for the treatment of a variety
CC of diseases. The present sequence represents a rabbit anti A33 antigen
CC antibody V region protein sequence which is given in an example from the
CC present invention.
XX
XX Sequence 109 AA;
SQ
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 GVSQYQQ 59
DB 32 GVSQYQQ 38
RESULT 49
AAB75151
ID AAB75151 standard; Protein; 109 AA.
XX
XX AC AAB75151;
XX

DT 08-AUG-2001 (first entry)
XX Rabbit anti A33 antigen antibody V region VL3 SEQ ID NO:22.
DE Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW immunoreact; anti A33 antigen antibody.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..34
FT /label= CDR1
FT Region 35..49
FT /label= FR2
FT Region 50..56
FT /label= CDR2
FT Region 57..88
FT /label= FR3
FT Region 89..99
FT /label= CDR3
FT Region 100..109
FT /label= FR4
XX WO200131065-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29026.
XX
XX 22-OCT-1999; 99US-0425638.
XX 04-APR-2000; 2000US-0543004.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX WPI; 2001-328657/34.
XX
XX Preparing humanized rabbit antibodies that specifically immunoreact
PT with a particular antigen using display technology for expressing
PT libraries of antibody domains and fine tuning variable domain regions -
XX
XX Example 4; Fig 1A; 62pp; English.
XX
XX The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarity determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human
CC mammalian antibodies, which can be used for the treatment of a variety
CC of diseases. The present sequence represents a rabbit anti A33 antigen
CC antibody V region protein sequence which is given in an example from the
CC present invention.
XX
XX Sequence 109 AA;
SQ
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 GVSQYQQ 59
DB 32 GVSQYQQ 38
RESULT 50
AAB75152
ID AAB75152 standard; Protein; 109 AA.
XX

IC AAB75152;
XX 08-AUG-2001 (first entry)
XX Humanised rabbit anti A33 antigen antibody V region VL SEQ ID NO:45.
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
XX immunoreact; anti A33 antigen antibody.
XX Oryctolagus cuniculus.
XX Synthetic.
XX Key Location/Qualifiers
XX Region 1..23
XX /label= FR1
XX Region 24..34
XX /label= CDR1
XX Region 35..49
XX /label= FR2
XX Region 50..56
XX /label= CDR2
XX Region 57..88
XX /label= FR3
XX Region 89..99
XX /label= CDR3
XX Region 100..109
XX /label= FR4
XX WO200131065-A1.
XX 03-MAY-2001.
XX 20-OCT-2000; 2000WO-US29026.
XX 22-OCT-1999; 99US-0425638.
XX 04-APR-2000; 2000US-0543004.
XX (SCRI) SCRIPPS RES INST.
XX Barbas CF, Rader C;
XX WPI; 2001-328657/34.
XX Preparing humanized rabbit antibodies that specifically immunoreact
XX with a particular antigen using display technology for expressing
XX libraries of antibody domains and fine tuning variable domain regions -
XX Example 6; Fig 1A; 62pp; English.
XX The present invention describes a method for preparing a humanised rabbit
XX antibody that specifically immunoreacts with a particular antigen. The
XX method comprises expressing a library of antibodies comprising one or
XX sequences that specifically immunoreact with the antigen grafted into
XX framework regions from humans, and selecting the antibodies that react
XX with the antigen. The method is useful for humanising non-human
XX mammalian antibodies, which can be used for the treatment of a variety
XX of diseases. The present sequence represents a humanised rabbit anti A33
XX antigen antibody V region protein sequence which is given in an example
XX from the present invention.
XX Sequence 109 AA;
XX Query Match 5.7%; Score 7; DB 22; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 53 GVSWTYQQ 59
XX DB 32 GVSWTYQQ 38
XX RESULT 51

AAB75153
ID AAB75153 standard; Protein; 109 AA.
XX
XX AAB75153;
AC 08-AUG-2001 (first entry)
DT
XX Human anti A33 antigen antibody V region VLA SEQ ID NO:39.
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
XX immunoreact; anti A33 antigen antibody.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Region 1..23
XX /label= FR1
XX Region 24..34
XX /label= CDR1
XX Region 35..49
XX /label= FR2
XX Region 50..56
XX /label= CDR2
XX Region 57..88
XX /label= FR3
XX Region 89..99
XX /label= CDR3
XX Region 100..109
XX /label= FR4
XX WO200131065-A1.
XX 03-MAY-2001.
XX 20-OCT-2000; 2000WO-US29026.
XX 22-OCT-1999; 99US-0425638.
XX 04-APR-2000; 2000US-0543004.
XX (SCRI) SCRIPPS RES INST.
XX Barbas CF, Rader C;
XX WPI; 2001-328657/34.
XX Preparing humanized rabbit antibodies that specifically immunoreact
XX with a particular antigen using display technology for expressing
XX libraries of antibody domains and fine tuning variable domain regions -
XX Example 6; Fig 1A; 62pp; English.
XX The present invention describes a method for preparing a humanised rabbit
XX antibody that specifically immunoreacts with a particular antigen. The
XX method comprises expressing a library of antibodies comprising one or
XX sequences that specifically immunoreact with the antigen grafted into
XX framework regions from humans, and selecting the antibodies that react
XX with the antigen. The method is useful for humanising non-human
XX mammalian antibodies, which can be used for the treatment of a variety
XX of diseases. The present sequence represents a human anti A33 antigen
XX antibody V region protein sequence which is given in an example from the
XX present invention.
XX Sequence 109 AA;
XX Query Match 5.7%; Score 7; DB 22; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 53 GVSWTYQQ 59
XX DB 32 GVSWTYQQ 38

```
RESULT 52
LAB75154
ID AAB75154 standard; Protein; 109 AA.
XX AC AAB75154;
XX DT 08-AUG-2001 (first entry)
XX DE Human anti A33 antigen antibody V region VLB SEQ ID NO:40.
XX GW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
XX KW immunoreact; anti A33 antigen antibody.
XX OS Homo sapiens.
XX FH Key
XX FT Region 1..23 /label= FR1
XX FT Region 24..34 /label= CDR1
XX FT Region 35..49 /label= FR2
XX FT Region 50..56 /label= CDR2
XX FT Region 57..88 /label= FR3
XX FT Region 89..99 /label= CDR3
XX FT Region 100..109 /label= FR4
XX PN WO200131065-A1.
XX PD 03-MAY-2001.
XX PF 20-OCT-2000; 2000WO-US29026.
XX PR 22-OCT-1999; 99US-0425638.
XX PR 04-APR-2000; 2000US-0543004.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX DR WPI; 2001-328657/34.
XX PT Preparing humanized rabbit antibodies that specifically immunoreact
XX PT with a particular antigen using display technology for expressing
XX PT libraries of antibody domains and fine tuning variable domain regions -
XX PS Example 6; Fig 1A; 62pp; English.
XX CC The present invention describes a method for preparing a humanised rabbit
XX CC antibody that specifically immunoreacts with a particular antigen. The
XX CC method comprises expressing a library of antibodies comprising one or
XX CC more complementarity determining region (CDR) from the variable domain
XX CC sequences that specifically immunoreact with the antigen grafted into
XX CC framework regions from humans, and selecting the antibodies that react
XX CC with the antigen. The method is useful for humanising non-human
XX CC mammalian antibodies, which can be used for the treatment of a variety
XX CC of diseases. The present sequence represents a human anti A33 antigen
XX CC antibody V region protein sequence which is given in an example from the
XX CC present invention.
XX SQ Sequence 109 AA;
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred.No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 GVSQYQQ 59
|||||
```

```
Db 32 GVSQYQQ 38
RESULT 53
AAB75155
ID AAB75155 standard; Protein; 109 AA.
XX AC AAB75155;
XX DT 08-AUG-2001 (first entry)
XX DE Human anti A33 antigen antibody V region VLB SEQ ID NO:41.
XX GW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
XX KW immunoreact; anti A33 antigen antibody.
XX OS Homo sapiens.
XX FH Key
XX FT Region 1..23 /label= FR1
XX FT Region 24..34 /label= CDR1
XX FT Region 35..49 /label= FR2
XX FT Region 50..56 /label= CDR2
XX FT Region 57..88 /label= FR3
XX FT Region 89..99 /label= CDR3
XX FT Region 100..109 /label= FR4
XX PN WO200131065-A1.
XX PD 03-MAY-2001.
XX PF 20-OCT-2000; 2000WO-US29026.
XX PR 22-OCT-1999; 99US-0425638.
XX PR 04-APR-2000; 2000US-0543004.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX DR WPI; 2001-328657/34.
XX PT Preparing humanized rabbit antibodies that specifically immunoreact
XX PT with a particular antigen using display technology for expressing
XX PT libraries of antibody domains and fine tuning variable domain regions -
XX PS Example 6; Fig 1A; 62pp; English.
XX CC The present invention describes a method for preparing a humanised rabbit
XX CC antibody that specifically immunoreacts with a particular antigen. The
XX CC method comprises expressing a library of antibodies comprising one or
XX CC more complementarity determining region (CDR) from the variable domain
XX CC sequences that specifically immunoreact with the antigen grafted into
XX CC framework regions from humans, and selecting the antibodies that react
XX CC with the antigen. The method is useful for humanising non-human
XX CC mammalian antibodies, which can be used for the treatment of a variety
XX CC of diseases. The present sequence represents a human anti A33 antigen
XX CC antibody V region protein sequence which is given in an example from the
XX CC present invention.
XX SQ Sequence 109 AA;
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred.No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Y 53 GVSXWYQQ 59
b 32 GVSXWYQQ 38

RESULT 54
AB75156
D AAB75156 standard; Protein; 109 AA.
X C AAB75156;
X T 08-AUG-2001 (first entry)
E Human anti A33 antigen antibody V region VLD SEQ ID NO:42.
X Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
W immunoreact; anti A33 antigen antibody.
X Homo sapiens.
H Key Location/Qualifiers
T Region 1..23 /label= FR1
T Region 24..34 /label= CDR1
T Region 35..49 /label= FR2
T Region 50..56 /label= CDR2
T Region 57..88 /label= FR3
T Region 89..99 /label= CDR3
T Region 100..109 /label= FR4
N WO200131065-A1.
D 03-MAY-2001.
X 20-OCT-2000; 2000WO-US29026.
F 22-OCT-1999; 99US-0425638.
R 04-APR-2000; 2000US-0543004.
R (SCRI) SCRIPPS RES INST.
A Barbas CF, Rader C;
I WPI; 2001-328657/34.
R Preparing humanized rabbit antibodies that specifically immunoreact
X with a particular antigen using display technology for expressing
X libraries of antibody domains and fine tuning variable domain regions -
X Example 6; Fig 1A; 62pp; English.
X The present invention describes a method for preparing a humanised rabbit
X antibody that specifically immunoreacts with a particular antigen. The
X method comprises expressing a library of antibodies comprising one or
X more complementarily determining region (CDR) from the variable domain
X sequences that specifically immunoreact with the antigen grafted into
X framework regions from humans, and selecting the antibodies that react
X with the antigen. The method is useful for humanising non-human
X mammalian antibodies, which can be used for the treatment of a variety
X of diseases. The present sequence represents a human anti A33 antigen
X antibody V region protein sequence which is given in an example from the
X present invention.
X Sequence 109 AA;
X Query Match 5.7%; Score 7; DB 22; Length 109;
X Best Local Similarity 100.0%; Pred. No. 39;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSXWYQQ 59
Db 32 GVSXWYQQ 38

RESULT 55
AAB75157
ID AAB75157 standard; Protein; 109 AA.
X C AAB75157;
X T 08-AUG-2001 (first entry)
E Human anti A33 antigen antibody V region VLE SEQ ID NO:43.
X Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
W immunoreact; anti A33 antigen antibody.
X Homo sapiens.
H Key Location/Qualifiers
T Region 1..23 /label= FR1
T Region 24..34 /label= CDR1
T Region 35..49 /label= FR2
T Region 50..56 /label= CDR2
T Region 57..88 /label= FR3
T Region 89..99 /label= CDR3
T Region 100..109 /label= FR4
N WO200131065-A1.
D 03-MAY-2001.
X 20-OCT-2000; 2000WO-US29026.
F 22-OCT-1999; 99US-0425638.
R 04-APR-2000; 2000US-0543004.
R (SCRI) SCRIPPS RES INST.
A Barbas CF, Rader C;
I WPI; 2001-328657/34.
R Preparing humanized rabbit antibodies that specifically immunoreact
X with a particular antigen using display technology for expressing
X libraries of antibody domains and fine tuning variable domain regions -
X Example 6; Fig 1A; 62pp; English.
X The present invention describes a method for preparing a humanised rabbit
X antibody that specifically immunoreacts with a particular antigen. The
X method comprises expressing a library of antibodies comprising one or
X more complementarily determining region (CDR) from the variable domain
X sequences that specifically immunoreact with the antigen grafted into
X framework regions from humans, and selecting the antibodies that react
X with the antigen. The method is useful for humanising non-human
X mammalian antibodies, which can be used for the treatment of a variety
X of diseases. The present sequence represents a human anti A33 antigen
X antibody V region protein sequence which is given in an example from the
X present invention.
X Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

53 GVSQYQQ 59
32 GVSQYQQ 38

RESULT 56
AB75158
D AAB75158 standard; Protein; 109 AA.
X
C AAB75158;
X
T 08-AUG-2001 (first entry)
X
E Human anti A33 antigen antibody V region VLF SEQ ID NO:44.
X
W Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
X immunoreact; anti A33 antigen antibody.
X
S Homo sapiens.
X
H Key Location/Qualifiers
T Region 1..23
T /label= FR1
T Region 24..34
T /label= CDR1
T Region 35..49
T /label= FR2
T Region 50..56
T /label= CDR2
T Region 57..88
T /label= FR3
T Region 89..99
T /label= CDR3
T Region 100..109
T /label= FR4
X WO200131065-A1.
X
X 03-MAY-2001.
X
X 20-OCT-2000; 2000WO-US29026.
X
X 22-OCT-1999; 99US-0425638.
X
X 04-APR-2000; 2000US-0543004.
X
X (SCRI) SCRIPPS RES INST.
X
X Barbas CF, Rader C;
X
X WPI; 2001-328657/34.
X
X Preparing humanized rabbit antibodies that specifically immunoreact
PT with a particular antigen using display technology for expressing
PT libraries of antibody domains and fine tuning variable domain regions -
X
X Example 6; Fig 1A; 62pp; English.
X
X The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarity determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human
CC mammalian antibodies, which can be used for the treatment of a variety
CC of diseases. The present sequence represents a human anti A33 antigen
CC antibody V region protein sequence which is given in an example from the
CC present invention.

SQ Sequence 109 AA;
Query Match 5.7%; Score 7; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

53 GVSQYQQ 59
32 GVSQYQQ 38

RESULT 57
AAR54277
ID AAR54277 standard; protein; 111 AA.
X
X AAR54277;
X
X 25-MAR-2003 (updated)
X 10-NOV-1994 (first entry)
X
X Anti-HIV gp41 immunoglobulin light chain V region clone GL 41 1.
X
X Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
X neutralisation; monoclonal antibody; light chain; variable region;
X framework region; complementarity determining region.
X
X Homo sapiens.
X
X Key Location/Qualifiers
T Region 1..23
T /label= FR1
T Region 24..35
T /label= CDR1
T Region 36..50
T /label= FR2
T Region 51..57
T /label= CDR2
T Region 58..89
T /label= FR3
T Region 90..97
T /label= CDR3
T Region 98..111
T /label= FR4
X WO9407922-A1.
X
X 14-APR-1994.
X
X 30-SEP-1993; 93WO-US09328.
X
X 30-SEP-1992; 92US-0954148.
X
X (SCRI) SCRIPPS RES INST.
X
X Barbas CF, Burton DR, Lerner RA;
X
X WPI; 1994-135516/16.
X
X New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
X
X Claim 11; Page 217; 248pp; English.
X
X Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC digisomic vector to produce a library of fragments. E.coli XLI
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VL region sequence AAR54277 neutralises HIV1
CC gp41.

CC (Updated on 25-MAR-2003 to correct PN field.)
CC Sequence 111 AA;
Query Match 5.7%; Score 7; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
82 DIPDRFS 88
58 DIPDRFS 64
RESULT 58
AA69089
D AAR69089 standard; Protein; 111 AA.
C AAR69089;
X
X
X 25-MAR-2003 (updated)
X 30-AUG-1995 (first entry)
X
X Anti-HIV Fab tat16 (VL1).
X HIV-1; human immunodeficiency virus type 1; AIDS; Tat protein;
X intracellular immunization; gene therapy; single chain antibody;
X Fab; antibody engineering; resistance; cell immunity.
X
X Homo sapiens.
X
X
X Key Location/Qualifiers
X 1..20
X Region /label= FR1
X 21..33
X Region /label= CDR1
X 34..48
X Region /label= FR2
X Misc-difference 42
X /notes "not known"
X Region 49..55
X /label= CDR2
X Region 56..87
X /label= FR3
X Region 88..100
X /label= CDR3
X Region 101..111
X /label= FR4
X
X WO9503832-A1.
X
X 09-FEB-1995.
X
X 28-JUL-1994; 94WO-US08448.
X
X 30-JUL-1993; 93US-0099870.
X
X (UYJE-) UNIV JEFFERSON THOMAS.
X
X Duan L, Pomerantz R;
X WPI; 1995-082039/11.
X
X Method for conducting gene therapy - comprises using recombinant
X gene encoding antibody binding antigen associated with a disease;
X useful for providing cell immunity.
X
X Example 11; Page 32-33; Table 2; 62pp; English.
X
X A phagemid library was constructed using lymphocyte RNA from
X a long-term asymptomatic HIV-1 positive donor. Heavy and light
X chain genes were cloned and a combinatorial library was prepared
X and screened to select antigen (HIV rev or tat) binders. Human
X soluble anti-HIV Fabs were obtained. Heavy chain VH sequences are

CC given in AAR69084-87, light chain VL in AAR69088-92 and light chain CL
CC in AAR69093-97.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 111 AA;
Query Match 5.7%; Score 7; DB 16; Length 111;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
83 IPDRFSA 89
57 IPDRFSA 63
RESULT 59
AAW01322
ID AAW01322 standard; Protein; 111 AA.
XX
XX AAW01322;
XX
XX 29-JAN-1997 (first entry)
XX
XX VL of Fab, GL 41 1, binds to HIV gp41.
XX Heavy chain; light chain; variable region; VH; monoclonal antibody;
XX WAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
XX virus infectivity assay; precursor gp160; immunocompetence; human;
XX anti-HIV antibody; detection; HIV infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX 1..23
XX Region /label= FR1
XX 24..35
XX Region /label= CDR1
XX 36..50
XX Region /label= FR2
XX 51..57
XX Region /label= CDR2
XX 58..89
XX Region /label= FR3
XX 90..97
XX Region /label= CDR3
XX 98..111
XX Region /label= FR4
XX
XX WO9602273-A1.
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US08743.
XX
XX 18-JUL-1994; 94US-0276852.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Burton DR, Lerner RA;
XX WPI; 1996-179601/18.
XX
XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
XX passive immunotherapy and detection of HIV infection.
XX
XX Example 3; Fig 19; 366pp; English.
XX
XX The sequences given in AAW01320-24 represent the light chain variable
XX regions (VH) of a series of antibody fragments (FAB's) which are
XX immunoreactive with HIV glycoprotein gp41. This sequence represents
XX the sequence of the clone, GL 41 1. These sequences represent light
XX chains which bind to the heavy light chain clones given in AAW01315-19.
XX A monoclonal antibody containing one of these Fab sequences may have the

CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/ml. The MAb may be used for determining immunocompetence of a human anti-HIV antibody and in the detection of HIV infection.

CC Sequence 111 AA;

Query Match 5.7%; Score 7; DB 17; Length 111;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

82 DIPDRFS 88
|||||
58 DIPDRFS 64

RESULT 60

AAW08738
ID AAW08738 standard; Protein; 111 AA.

AAW08738;

08-AUG-1997 (first entry)

Human anti-HIV Fab amino acid sequence tat16(VL1).

Gene therapy; antibody; immunisation; human immunodeficiency virus; HIV; human T-cell leukaemia virus.

Human Immunodeficiency Virus Type-1.

Key Location/Qualifiers

Region 1..20

Region 21..33

Region 34..48

Region 49..55

Region 56..87

Region 87..100

Region 101..111

Misc-difference 42

/label= FR1

/label= CDR1

/label= FR2

/label= CDR2

/label= FR3

/label= CDR3

/label= FR4

/label= Unspecified

WO9637234-A1.

28-NOV-1996.

23-MAY-1996; 96WO-US07393.

23-MAY-1995; 95US-0447610.

(UVEJ-) UNIV JEFFERSON THOMAS.

Duan L, Pomerantz RJ;

WPI; 1997-020948/02.

Improved gene therapy using recombinant gene coding for an antibody - for intracellular immunisation against pathogens recognised by the antibody, esp. human immunodeficiency virus HIV-1

Example 11; Page 58; 213pp; English.

The present sequence is a human anti-HIV Fab light chain VL sequence. A novel gene therapy method has been produced, where a recombinant (rec) gene is introduced into the cells of a mammal. The method is improved by using a rec gene encoding an antibody (Ab) (e.g. the

CC present sequence) that is selectively specific for an intracellular (IC) antigen associated with a disease. The method is used to prevent or halt the progress of a disease by IC immunisation. Specifically, the Ab can be used to inhibit the replication of a virus, such as human T-cell leukaemia virus or especially HIV-1, or of other pathogens, e.g. bacteria, fungi. The method provides immunity before or after the development of the disease and can be used to control the severity of the disease.

CC Sequence 111 AA;

Query Match 5.7%; Score 7; DB 18; Length 111;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

83 IPDRFSA 89

|||||

57 IPDRFSA 63

RESULT 61

AAAY95172

ID AAY95172 standard; Protein; 111 AA.

AAAY95172;

30-JUN-2000 (first entry)

Anti-gp41 light chain variable region from clone DL 41 1.

Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise; reduce HIV infection; diagnosis; immunotherapy; HIV induced disease; glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

Homo sapiens.

AU9948756-A.

17-FEB-2000.

16-SEP-1999; 99AU-0048756.

16-SEP-1999; 99AU-0048756.

(SCRI) SCRIPPS RES INST.

Burton DR, Barbas CF, Lerner RA;

WPI; 2000-293393/26.

Novel human monoclonal antibodies which immunoreact with and neutralise human immunodeficiency virus useful for treating HIV infections

Disclosure; Figure 19; 366pp; English.

The present sequence represents a fragment of an anti-human immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV mature glycoprotein gp120 preferentially over HIV precursor glycoprotein gp160 and neutralises HIV and which reduces HIV infectivity titre in an in vitro virus infectivity assay by 50%, at a concentration of less than 700 ng/ml. The antibodies are used as reagents for the diagnosis and immunotherapy of HIV induced disease. They are useful as neutralising field isolates and provide useful information regarding the immunocompetence of an immune response in HIV infected patients. The monoclonal antibodies are useful for producing anti-idiotypic antibodies which can be used to screen human monoclonal antibodies to identify whether the antibody has the same binding specificity as the antibodies of the invention. The neutralising antibodies define new epitopes on the HIV gp120 and gp41 glycoproteins, thus increasing the availability of new immunotherapeutic human monoclonal antibodies. A major advantage of the monoclonal antibodies derives from the fact that they are encoded by a human polynucleotide sequence. Thus in vivo use of the monoclonal

antibodies for diagnosis and immunotherapy of HIV induced disease greatly reduces the problems of significant host immune response to the passively administered antibodies which is a problem commonly encountered when monoclonal antibodies of xenogeneic or chimeric derivation are utilized. An additional major advantage of the monoclonal antibodies described derives from the fact that they immunoreact with a unique determinant present on mature HIV glycoprotein gp120. This class of antibodies is particularly effective at neutralising field isolates of HIV.

Sequence 111 AA;
Query Match 5.7%; Score 7; DB 21; Length 111;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 82 DIPDRFS 88
b 58 DIPDRFS 64

RESULT 62
AY98281
D AAY98281 standard; Protein; 111 AA.
X C
X C AAY98281;
X T 04-JUL-2000 (first entry)
X E Anti-gp41 light chain variable region from clone DL 41 1.
X W Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
W human immunodeficiency virus type 1; HIV-1; infectivity titre;
W passive immunotherapy; reduce severity; HIV-induced disease;
W immunocompetence; active immunisation.
X S Homo sapiens.
X X AU9948754-A.
X N 17-FEB-2000.
X D 16-SEP-1999; 99AU-0048754.
X F 16-SEP-1999; 99AU-0048754.
X R (SCRI) SCRIPPS RES INST.
X A Burton DR, Barbas CF, Lerner RA;
X Z WPI; 2000-246867/22.
X R Human neutralizing monoclonal antibodies to human immunodeficiency virus (HIV) used for providing passive immunotherapy to HIV are specific for glycoprotein-120
X PT Disclosure; Figure 19; 374pp; English.
X PS
X CC This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable of reducing an HIV infectivity titre in an in vitro virus infectivity assay by 50% at a concentration of less than 70 ng/ml. The method for the production of the antibody comprises:
CC (a) providing a first polynucleotide encoding a heavy chain immunoglobulin amino acid sequence (which does not comprise the sequence represented by AAY98206) and a second polynucleotide encoding a light chain immunoglobulin amino acid sequence;
CC (b) inserting the first and second polynucleotide sequences into a host cell;
CC (c) maintaining the host cell in conditions which allow the amino acid sequences encoded by the polynucleotides to be expressed in the host cell; and
CC (d) isolating the antibody comprising the heavy and light chain

immunoglobulin amino acid sequences from the host cell.
CC The anti-HIV gp-120 monoclonal antibody is used for providing passive immunotherapy to HIV in a human. They can be administered to high-risk patients to reduce the likelihood and/or severity of HIV-induced disease and to patients who are already HIV-infected. The antibodies are used for neutralising field isolates which provides information about the immunocompetence of an immune response in HIV patients, for detecting HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for producing anti-idiotypic antibodies which can be used for active immunisation and to screen human monoclonal antibodies to identify those with the same binding specificity and to monitor the course of HIV disease therapy by measuring the changes in concentration of HIV present in the body or in body fluids by immunoassay. The anti-HIV gp-120 monoclonal antibodies are encoded by a human polynucleotide sequence and when used in vivo for diagnosis and immunotherapy of HIV-induced disease reduce the problems of significant host immune response to the antibodies associated with monoclonal antibodies of xenogeneic or chimeric derivation.

Sequence 111 AA;
Query Match 5.7%; Score 7; DB 21; Length 111;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 DIPDRFS 88
DB 58 DIPDRFS 64

RESULT 63
ABG64978
ID ABG64978 standard; Protein; 120 AA.
X X
X X ABG64978;
X X 27-AUG-2002 (first entry)
X DT Human albumin fusion protein #1653.
X DE
X X Albumin fusion protein; therapeutic protein X; human albumin; HA;
X K human serum albumin; HSA; cancer; reproductive disorder;
X W digestive disorder; immune disorder; endocrine disorder;
X W haematopoietic disorder; neural disorder; connective disorder;
X W cytostatic; antifertility; antiinflammatory; antitumor;
X W immunomodulator; anti-HIV; antidiabetic; haemostatic; neuroleptic;
X W neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
X W osteopathic; antiarthritic.

Homo sapiens.
OS Synthetic.
X OS
X X WO200177137-A1.
X DN 18-OCT-2001.
X X
X X 12-APR-2001; 2001WO-US11988.
X PF
X X 12-APR-2000; 2000US-229358P.
X X 25-APR-2000; 2000US-159384P.
X X 21-DEC-2000; 2000US-256931P.
X X (HUMA-) HUMAN GENOME SCI INC.
X X Rosen CA, Haseltine WA;
X PI WPI; 2002-010886/01.
X DR
X X New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein -
X PT Claim 1; Page 1651; 2102pp; English.
X PS
X X

CC The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA), also known as human serum albumin (HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological C in vitro/in vivo activity. The protein is useful for treating and C diagnosing disorders such as cancer, reproductive disorders, digestive C disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders C (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders C (e.g. diabetes), haematopoietic disorders, neural disorders C (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, C encephalomyelitis, meningitis, schizophrenia), and connective disorders C (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin C fusion proteins of the invention.

XX Sequence 120 AA;

Query Match 5.7%; Score 7; DB 23; Length 120;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 28 LLVFPGQ 34
 |||||
 Db 11 LLVFPGQ 17

RESULT 64
 ABG64980
 D ABG64980 standard; Protein; 120 AA.

XX AAE21465;
 XX 01-JUL-2002 (first entry)
 XX Human gene 14 encoded secreted protein HDPXL05, SEQ ID NO:81.
 XX Human; secreted protein; gene therapy; autoimmune disease; vitamin;
 XX rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast;
 XX liver; cardiovascular; cardiac arrest; cerebrovascular; infection;
 XX cerebral ischaemia; angiogenesis; nervous system; Alzheimer's disease;
 XX ocular; corneal infection; wound healing; neuroprotective; skin aging;
 XX transplantation; chemotaxis; food additive; preservative; vulnary;
 XX storage capability; mineral; cofactor; immunosuppressive; cytostatic;
 XX antiproliferative; cardiant; vasotropic; cerebroprotective; nootropic;
 XX fungicide; ophthalmological; sunburn; virucide; antibacterial.

XX Homo sapiens.
 XX Key Location/Qualifiers
 XX Peptide 1..20
 XX /label= Signal_peptide
 XX Protein 21..120
 XX /label= Mature_secreted_protein
 XX WO200177137-A1.
 XX 18-OCT-2001.
 XX 12-APR-2001; 2001WO-US11988.
 XX 12-APR-2000; 2000US-229358P.
 XX 25-APR-2000; 2000US-19384P.
 XX 21-DEC-2000; 2000US-256931P.
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Haseltine WA;
 XX WPI; 2002-010886/01.
 XX New fusion protein for treating disease e.g. diabetes comprises an
 XX albumin fused to a therapeutic protein -
 XX Claim 1; Page 1652; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a
 XX therapeutic protein X and human albumin (HA), also known as human serum
 XX albumin, HSA). The proteins are useful for treating a disease or
 XX disorder that may be modulated by therapeutic protein X. The albumin

CC extends the shelf-life of protein X, and may increase its biological
 CC in vitro/in vivo activity. The protein is useful for treating and
 CC diagnosing disorders such as cancer, reproductive disorders, digestive
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
 CC (e.g. diabetes), haematopoietic disorders, neural disorders
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
 CC fusion proteins of the invention.

XX Sequence 120 AA;

Query Match 5.7%; Score 7; DB 23; Length 120;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LLVFPGQ 34
 |||||
 Db 11 LLVFPGQ 17

RESULT 65
 AAE21465
 ID AAE21465 standard; Protein; 120 AA.

XX AAE21465;
 XX 01-JUL-2002 (first entry)
 XX Human gene 14 encoded secreted protein HDPXL05, SEQ ID NO:81.
 XX Human; secreted protein; gene therapy; autoimmune disease; vitamin;
 XX rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast;
 XX liver; cardiovascular; cardiac arrest; cerebrovascular; infection;
 XX cerebral ischaemia; angiogenesis; nervous system; Alzheimer's disease;
 XX ocular; corneal infection; wound healing; neuroprotective; skin aging;
 XX transplantation; chemotaxis; food additive; preservative; vulnary;
 XX storage capability; mineral; cofactor; immunosuppressive; cytostatic;
 XX antiproliferative; cardiant; vasotropic; cerebroprotective; nootropic;
 XX fungicide; ophthalmological; sunburn; virucide; antibacterial.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 1..20
 XX /label= Signal_peptide
 XX Protein 21..120
 XX /label= Mature_secreted_protein
 XX WO200224719-A1.

XX 28-MAR-2002.
 XX 17-JAN-2001; 2001WO-US01565.
 XX 20-SEP-2000; 2000US-234210P.
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
 XX Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M,
 XX Ni J;
 XX WPI; 2002-258042/30.
 XX N-PSDB; AAD33825.

XX New nucleic acid molecules encoding 21 human secreted proteins for
 XX diagnosing or treating e.g. autoimmune diseases, hyperproliferative
 XX disorders, and cardiovascular disorders, and used as food additives or
 XX preservatives -
 XX Claim 11; Page 477; 519pp; English.

DS Homo sapiens.
PX KN WO200155448-A1.
PX KX
PD PD 02-AUG-2001.
PF KX
PF KX 17-JAN-2001; 2001WO-US01333.
PX 31-JAN-2000; 2000US-0179065.
PX 04-FEB-2000; 2000US-0180628.
PX 24-FEB-2000; 2000US-0184664.
PX 02-MAR-2000; 2000US-0186350.
PX 16-MAR-2000; 2000US-0189874.
PX 17-MAR-2000; 2000US-0190076.
PX 18-APR-2000; 2000US-0198123.
PX 19-MAY-2000; 2000US-0205515.
PX 07-JUN-2000; 2000US-0209467.
PX 28-JUN-2000; 2000US-02114886.
PX 30-JUN-2000; 2000US-0215135.
PX 07-JUL-2000; 2000US-0216647.
PX 07-JUL-2000; 2000US-0216880.
PX 11-JUL-2000; 2000US-0217487.
PX 11-JUL-2000; 2000US-0217496.
PX 14-JUL-2000; 2000US-0218290.
PX 26-JUL-2000; 2000US-0220963.
PX 26-JUL-2000; 2000US-0220964.
PX 14-AUG-2000; 2000US-0224518.
PX 14-AUG-2000; 2000US-0224519.
PX 14-AUG-2000; 2000US-0225213.
PX 14-AUG-2000; 2000US-0225214.
PX 14-AUG-2000; 2000US-0225266.
PX 14-AUG-2000; 2000US-0225267.
PX 14-AUG-2000; 2000US-0225270.
PX 14-AUG-2000; 2000US-0225447.
PX 14-AUG-2000; 2000US-0225757.
PX 14-AUG-2000; 2000US-0225758.
PX 14-AUG-2000; 2000US-0225759.
PX 18-AUG-2000; 2000US-0226279.
PX 22-AUG-2000; 2000US-0226681.
PX 22-AUG-2000; 2000US-0226868.
PX 22-AUG-2000; 2000US-0227182.
PX 23-AUG-2000; 2000US-0227009.
PX 30-AUG-2000; 2000US-0228924.
PX 01-SEP-2000; 2000US-0228287.
PX 01-SEP-2000; 2000US-0229343.
PX 01-SEP-2000; 2000US-0229344.
PX 01-SEP-2000; 2000US-0229345.
PX 05-SEP-2000; 2000US-0229509.
PX 06-SEP-2000; 2000US-0229513.
PX 06-SEP-2000; 2000US-0230437.
PX 06-SEP-2000; 2000US-0230438.
PX 08-SEP-2000; 2000US-0231242.
PX 08-SEP-2000; 2000US-0231243.
PX 08-SEP-2000; 2000US-0231244.
PX 08-SEP-2000; 2000US-0231413.
PX 08-SEP-2000; 2000US-0231414.
PX 08-SEP-2000; 2000US-0232080.
PX 08-SEP-2000; 2000US-0232081.
PX 12-SEP-2000; 2000US-0231968.
PX 14-SEP-2000; 2000US-0232397.
PX 14-SEP-2000; 2000US-0232398.
PX 14-SEP-2000; 2000US-0232399.
PX 14-SEP-2000; 2000US-0232400.
PX 14-SEP-2000; 2000US-0232401.
PX 14-SEP-2000; 2000US-0233063.
PX 14-SEP-2000; 2000US-0233064.
PX 14-SEP-2000; 2000US-0233065.
PX 21-SEP-2000; 2000US-0234223.
PX 21-SEP-2000; 2000US-0234274.
PX 25-SEP-2000; 2000US-0234997.
PX 25-SEP-2000; 2000US-0234998.
PX 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251989.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0254097.
XX XX (HUMA-) HUMAN GENOME SCI INC.
PA

X I Rosen CA, Barash SC, Ruben SM;
X R WPI; 2001-476224/51.
X R N-PSDB; AAS28071.
X T Isolated polypeptide for treating, preventing and/or prognosing
X T disorders related to the respiratory system including respiratory
X T cancers and also for testing and detection e.g. diagnosis -
X S Claim 11; SEQ ID No 505; 546pp; English.
X C The present invention relates to the isolation of novel human
X C respiratory antigens, and cDNA (AAS27869-AAS28159) and genomic
X C sequences encoding for these polypeptides. The sequences of the
X C invention are useful for preventing, treating and/or prognosing
X C disorders related to the respiratory system including throat
X C disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis),
X C lung disorders e.g. pneumonia, allergic disorders e.g. asthma,
X C pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of
X C the respiratory tissues e.g. lung cancer. The polynucleotide sequences
X C of the invention are useful in gene therapy and antisense therapy.
X C AAU17685-AAU17975 represent novel human respiratory antigens.
X C Note: The sequence data for this patent did not form part of the printed
X C specification, but was obtained in electronic format directly from WIPO
X C at ftp.wipo.int/pub/published_pct_sequences.

X Q Sequence 121 AA;
Query Match 5.7%; Score 7; DB 22; Length 121;
Best Local Similarity 100.0%; Pred.No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 27 ALLVFFG 33
b 55 ALLVFFG 61
|||||

RESULT 68
BG18228
D ABG18228 standard; Protein; 122 AA.
X C ABG18228;
X T 18-FEB-2002 (first entry)
X C Novel human diagnostic protein #18219.
X Human; chromosome mapping; gene mapping; gene therapy; forensic;
X food supplement; medical imaging; diagnostic; genetic disorder.
X Homo sapiens.
X WO200175067-A2.
X 11-OCT-2001.
X 30-MAR-2001; 2001WO-US08631.
X 31-MAR-2000; 2000US-0540217.
X 23-AUG-2000; 2000US-0649167.
X (HYSE-) HYSEQ INC.
X Drmanac RT, Liu C, Tang YT;
X WPI; 2001-639362/73.
X N-PSDB; AAS82415.
X New isolated polynucleotide and encoded polypeptides, useful in
X diagnostics, forensics, gene mapping, identification of mutations
X responsible for genetic disorders or other traits and to assess
X biodiversity -
X Claim 20; SEQ ID No 43246; 103pp; English.

XX PS Claim 20; SEQ ID No 48587; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (III) and its binding partners are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX Q Sequence 122 AA;

Query Match 5.7%; Score 7; DB 22; Length 122;
Best Local Similarity 100.0%; Pred.No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 ABRYLTY 70
Db 103 ABRYLTY 109
|||||

RESULT 69
ABG12887
ID ABG12887 standard; Protein; 161 AA.
XX AC ABG12887;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #12878.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS77074.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX Claim 20; SEQ ID No 43246; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) is useful for generating antibodies against it, detecting or
 CC imaging of sites expressing (II). (I) and (II) are useful in medical
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 161 AA;
 CC Query Match 5.7%; Score 7; DB 22; Length 161;
 CC Best Local Similarity 100.0%; Pred. No. 54;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQR 60
 DB 75 VSWYQQR 81
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RESULT 70
 ABG19759
 ID ABG19759 standard; Protein; 182 AA.

XX AC ABG19759;
 XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #19750.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS93946.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 20; SEQ ID No 50118; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC N-PSDB; ABA09019.

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 182 AA;

XX Query Match 5.7%; Score 7; DB 22; Length 182;
 XX Best Local Similarity 100.0%; Pred. No. 60;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 PRYLLEY 71
 |||||

DB 65 PRYLLEY 71
 |||||

RESULT 71
 ABB11775
 ID ABB11775 standard; peptide; 211 AA.

XX AC ABB11775;

XX DT 11-JAN-2002 (first entry)

XX DE Human 14274 receptor protein homologue, SEQ ID NO:2145.

XX KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;

XX KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

XX KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;

XX KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;

XX KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;

XX KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.

XX OS Homo sapiens.

XX PN WO200157188-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US03800.

XX PR 03-FEB-2000; 2000US-0496914.

XX PR 27-APR-2000; 2000US-0560875.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-457740/49.

XX DR N-PSDB; ABA09019.

PT Protein 2..107 /note= "preferred light chain for use in constructs
 TT /note= Of the invention (Claim 15)"
 TT Domain 2..95 /label= VKSEGMENT
 TT Domain 96..108 /note= "variable segment of the kappa light chain"
 TT Domain 109..213 /label= JK
 TT Domain 109..213 /note= "kappa light chain joining segment"
 TT Region /label= CK
 TT Region /note= "kappa light chain constant segment"
 TT Region 2..22 /label= FR1
 TT Region /note= "framework region 1"
 TT Region 23..34 /label= CDR1
 TT Region /note= "complementarity determining region 1"
 TT Region 35..49 /label= FR2
 TT Region /note= "framework region 2"
 TT Region 50..56 /label= CDR2
 TT Region /note= "complementarity determining region 2"
 TT Region 57..88 /label= FR3
 TT Region /note= "framework region 3"
 TT Region 89..97 /label= CDR3
 TT Region /note= "complementarity determining region 3"
 TT Region 98..108 /label= FR4
 TT Region /note= "framework region 4"
 TT WO9639186-A1.
 TT 12-DEC-1996.
 TT 05-JUN-1996; 96WO-US08756.
 TT 06-JUN-1995; 95US-0472688.
 TT (CEDA-) CEDARS SINAI MEDICAL CENT.
 TT (REGC) UNIV CALIFORNIA.
 TT Braun J, Eggena MP, Targan SR;
 TT WPI; 1997-042866/04.
 TT N-PSDB; AAT44090.
 TT Antibody material associated with ulcerative colitis - comprising
 TT anti-neutrophil cytoplasmic antibody, characterised by perinuclear
 TT neutrophil staining pattern
 TT Disclosure; Page 117-118; 145pp; English.
 TT A polypeptide (AAW07615) comprises the light chain of recombinant
 TT UCPANCA Fab clone 5-3. Anti-neutrophil cytoplasmic antibodies
 TT characterised by perinuclear neutrophil staining pattern (PANCA)
 TT associated with ulcerative colitis (UC) were recombinantly produced
 TT and characterised using a phase display technique. Libraries of VH-
 TT and VL-encoding DNA homologues having the immunoreactivity of
 TT UCPANCA antigen were created. Recombinant UCPANCA Fab clones 5-3
 TT and 5-4 were generated (see also AAW07613-16). These can be used in
 TT methods for screening for UCPANCA and for isolating UCPANCA
 TT antigens.
 TT Sequence 214 AA;
 TT Query Match 5.7%; Score 7; DB 18; Length 214;
 TT Best Local Similarity 100.0%; Pred. No. 70;
 TT Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89
 DB 58 IPDRFSA 64
 RESULT 74
 AAW64671
 ID AAW64671 standard; Protein; 214 AA.
 XX AAW64671;
 XX 11-NOV-1998 (first entry)
 DT Human UC pANCA monoclonal antibody NANUC-1 light chain.
 DE NANUC-1; NANUC-2; UC pANCA; monoclonal antibody; ulcerative colitis;
 KW UC pANCA secretory vesicle antigen; secretory vesicle membrane; UC;
 KW mast cell; neuroendocrine cell; tolerogenic; autoantibody.
 XX Homo sapiens.
 OS WO9837415-A1.
 PN 27-AUG-1998.
 PD 06-AUG-1997; 97WO-US13059.
 PF 20-FEB-1997; 97US-0804106.
 PR (CEDA-) CEDARS SINAI MEDICAL CENT.
 XX (REGC) UNIV CALIFORNIA.
 XX Braun J, Eggena M, Gordon LK, Targan SR;
 XX WPI; 1998-467728/40.
 DR N-PSDB; AAV51395.
 XX New ulcerative colitis pANCA secretory vesicle antigen - is
 PT immuno-reactive with NANUC-1 and NANUC-2 and is expressed in
 PT secretory vesicle membrane
 PT Disclosure; Pages 62-63; 83pp; English.
 XX This represents the light chain of human NANUC-1, a representative
 CC UC pANCA monoclonal antibody. The invention provides a pure ulcerative
 CC colitis (UC) pANCA secretory vesicle antigen, comprising a protein
 CC immunoreactive with NANUC-1 and NANUC-2 antibodies, and characterised by
 CC being selectively expressed in secretory vesicle membrane, in mast and/or
 CC neuroendocrine cells. The UC pANCA secretory vesicle antigen can be used
 CC in compositions or as tolerogenic fragment, combined with a tolerogising
 CC molecule for the diagnosis of UC, or for detecting susceptibility to UC.
 CC Tolerance may be induced in a pANCA positive patient by administration of
 CC a substantially pure UC pANCA secretory vesicle antigen or a tolerogenic
 CC fragment, such that the level of autoantibodies reactive with the antigen
 CC in the patient is reduced. Administration of this antigen prevents the
 CC formation of UC.
 XX SQ Sequence 214 AA;
 XX Query Match 5.7%; Score 7; DB 19; Length 214;
 XX Best Local Similarity 100.0%; Pred. No. 70;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 83 IPDRFSA 89
 DB 58 IPDRFSA 64
 RESULT 75
 RAY34039
 ID AAY34039 standard; Protein; 214 AA.
 XX AAY34039;
 AC AAY34039;

23-NOV-1999 (first entry)
 NANUC-2 antibody light chain.
 Ulcerative colitis; histone; H1-like antigen; porin antigen; human; Bacteroides antigen; inflammatory bowel disease; IBD; PANCA; diagnosis; perinuclear anti-neutrophil cytoplasmic antibody; isoform; NANUC-2.
 Homo sapiens.
 WO9945955-A1.
 16-SEP-1999.
 12-MAR-1999; 99WO-US05492.
 12-MAR-1998; 98US-0041889.
 (REGC) UNIV CALIFORNIA.
 Braun J, Cohavy O;
 WPI; 1999-551215/46.
 N-PSDB; AAX91123.
 Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis -
 Disclosure; Page 109-110; 134pp; English.
 The invention provides a method for the diagnosis, prevention and treatment of ulcerative colitis (UC) using histone H1-like antigen, a porin antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a complex of the histone H1-like antigen, or the PANCA-reactive fragment, and antibody to the histone H1-like antigen; and (3) detecting the presence or absence of the complex; where the presence of the complex indicates that the subject has UC. The PANCA-reactive histone H1-like antigen, porin antigen and Bacteroides antigen are useful in the diagnosis, prevention and treatment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence represents the light chain of NANUC-2 antibody.
 Sequence 214 AA;
 Query Match 5.7%; Score 7; DB 20; Length 214;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 83 IPDRFSA 89
 58 IPDRFSA 64

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job time : 49 secs

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title: US-09-981-876-200

arfect score: 123

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	123	100.0	123	4	Sequence 117, Appl
2	8	6.5	689	4	Sequence 2, Appl
3	7	5.7	52	1	Sequence 43, Appl
4	7	5.7	103	2	Sequence 71, Appl
5	7	5.7	104	1	Sequence 92, Appl
6	7	5.7	104	1	Sequence 92, Appl
7	7	5.7	104	1	Sequence 92, Appl
8	7	5.7	104	1	Sequence 92, Appl
9	7	5.7	109	1	Sequence 92, Appl
10	7	5.7	109	4	Sequence 20, Appl
11	7	5.7	109	4	Sequence 21, Appl
12	7	5.7	109	4	Sequence 22, Appl
13	7	5.7	109	4	Sequence 39, Appl
14	7	5.7	109	4	Sequence 40, Appl
15	7	5.7	109	4	Sequence 41, Appl
16	7	5.7	109	4	Sequence 42, Appl
17	7	5.7	109	4	Sequence 43, Appl
18	7	5.7	109	4	Sequence 44, Appl
19	7	5.7	109	4	Sequence 45, Appl
20	7	5.7	109	4	Sequence 20, Appl
21	7	5.7	109	4	Sequence 21, Appl
22	7	5.7	109	4	Sequence 22, Appl
23	7	5.7	109	4	Sequence 39, Appl
24	7	5.7	109	4	Sequence 40, Appl
25	7	5.7	109	4	Sequence 41, Appl
26	7	5.7	109	4	Sequence 42, Appl
27	7	5.7	109	4	Sequence 43, Appl

28	7	5.7	109	4	US-09-543-004-44	Sequence 44, Appl
29	7	5.7	109	4	US-09-543-004-45	Sequence 45, Appl
30	7	5.7	109	5	PCT-US93-08786-23	Sequence 23, Appl
31	7	5.7	111	1	US-08-276-852-149	Sequence 149, Appl
32	7	5.7	111	1	US-08-899-575-149	Sequence 149, Appl
33	7	5.7	111	1	US-08-899-575-149	Sequence 149, Appl
34	7	5.7	111	5	PCT-US95-08743-149	Sequence 149, Appl
35	7	5.7	214	2	US-08-480-753-6	Sequence 6, Appl
36	7	5.7	214	3	US-09-041-889-11	Sequence 11, Appl
37	7	5.7	214	4	US-08-337-058-11	Sequence 11, Appl
38	7	5.7	214	4	US-09-417-264-11	Sequence 6418, Appl
39	7	5.7	255	4	US-08-328-352-6418	Sequence 140, Appl
40	7	5.7	270	4	US-09-266-965-140	Sequence 21249, A
41	7	5.7	613	4	US-09-252-991A-21249	Sequence 2, Appl
42	7	5.7	934	1	US-08-457-176-2	Sequence 1, Appl
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44	7	5.7	934	3	US-08-709-784-1	Sequence 1, Appl
45	7	5.7	934	4	US-09-651-656-3	Sequence 3, Appl
46	7	5.7	934	4	US-09-650-855-3	Sequence 3, Appl
47	7	5.7	934	4	US-09-708-200-13	Sequence 13, Appl
48	7	5.7	1010	4	US-09-512-250C-31	Sequence 31, Appl
49	7	5.7	1039	4	US-09-252-991A-28966	Sequence 28966, A
50	6	4.9	12	3	US-08-747-599A-17	Sequence 17, Appl
51	6	4.9	18	1	US-08-476-405A-1	Sequence 1, Appl
52	6	4.9	20	3	US-08-658-136-23	Sequence 23, Appl
53	6	4.9	21	4	US-09-680-454-102	Sequence 102, Appl
54	6	4.9	53	1	US-08-162-102C-44	Sequence 44, Appl
55	6	4.9	54	3	US-08-851-843A-183	Sequence 183, Appl
56	6	4.9	54	3	US-08-974-549A-302	Sequence 302, Appl
57	6	4.9	54	3	US-08-854-050-183	Sequence 183, Appl
58	6	4.9	54	4	US-09-430-323-183	Sequence 183, Appl
59	6	4.9	64	2	US-07-765-179B-19	Sequence 19, Appl
60	6	4.9	67	2	US-08-273-146-67	Sequence 67, Appl
61	6	4.9	72	4	US-08-003-198A-17	Sequence 17, Appl
62	6	4.9	82	1	US-08-476-405A-25	Sequence 25, Appl
63	6	4.9	92	1	US-08-181-492B-27	Sequence 27, Appl
64	6	4.9	92	5	PCT-US95-00408-27	Sequence 27, Appl
65	6	4.9	94	4	US-09-732-210-818	Sequence 818, Appl
66	6	4.9	96	1	US-08-488-113B-158	Sequence 158, Appl
67	6	4.9	96	1	US-08-477-484B-158	Sequence 158, Appl
68	6	4.9	96	1	US-08-107-669D-22	Sequence 22, Appl
69	6	4.9	96	1	US-08-472-788A-22	Sequence 22, Appl
70	6	4.9	96	2	US-08-477-531B-22	Sequence 22, Appl
71	6	4.9	96	2	US-08-646-360-158	Sequence 158, Appl
72	6	4.9	96	2	US-08-082-842A-22	Sequence 22, Appl
73	6	4.9	96	3	US-08-839-765-158	Sequence 158, Appl
74	6	4.9	96	3	US-09-136-389-158	Sequence 158, Appl
75	6	4.9	96	4	US-09-610-838-158	Sequence 35, Appl
76	6	4.9	97	2	US-08-665-202-35	Sequence 35, Appl
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78	6	4.9	98	2	US-08-665-202-37	Sequence 37, Appl
79	6	4.9	98	4	US-09-315-574-37	Sequence 16637, A
80	6	4.9	99	4	US-09-253-991A-16637	Sequence 100, Appl
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82	6	4.9	104	1	US-08-488-113B-153	Sequence 153, Appl
83	6	4.9	104	1	US-08-477-484B-153	Sequence 153, Appl
84	6	4.9	104	1	US-08-107-669D-17	Sequence 17, Appl
85	6	4.9	104	1	US-08-472-788A-17	Sequence 17, Appl
86	6	4.9	104	1	US-08-898-575-100	Sequence 100, Appl
87	6	4.9	104	1	US-08-898-575-100	Sequence 100, Appl
88	6	4.9	104	2	US-08-477-531B-17	Sequence 17, Appl
89	6	4.9	104	2	US-08-646-360-153	Sequence 153, Appl
90	6	4.9	104	2	US-08-273-146-63	Sequence 63, Appl
91	6	4.9	104	2	US-08-082-842A-17	Sequence 17, Appl
92	6	4.9	104	3	US-08-839-765-153	Sequence 153, Appl
93	6	4.9	104	3	US-09-136-389-153	Sequence 153, Appl
94	6	4.9	104	3	US-09-240-274-69	Sequence 69, Appl
95	6	4.9	104	3	US-09-240-274-69	Sequence 2, Appl
96	6	4.9	104	4	US-08-793-450-2	Sequence 153, Appl
97	6	4.9	104	4	US-09-610-838-153	Sequence 100, Appl
98	6	4.9	104	5	PCT-US95-08743-100	Sequence 157, Appl
99	6	4.9	105	1	US-08-488-113B-157	Sequence 157, Appl
100	6	4.9	105	1	US-08-477-484B-157	Sequence 157, Appl

ALIGNMENTS

RESULT 1

IS-09-996-243-117

Sequence 117, Application US/09996243

Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C13

CURRENT APPLICATION NUMBER: US/09/996,243

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03

PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

PRIOR FILING DATE: 1998-06-04

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252

PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090594
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 123; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred.No. 3.6e-116;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2y 1 MACCLFLMGLTSLVSQTVLQALDALLVPCQVQLSCTLSPOHVTIRDYGVSWYQOR 60
 3b 1 MACCLFLMGLTSLVSQTVLQALDALLVPCQVQLSCTLSPOHVTIRDYGVSWYQOR 60
 2y 61 AGSAPRYLLYRSDEHRRPADIPDRFSAKBAHNAACVLTISPVPEDDADYICSVGVG 120
 3b 61 AGSAPRYLLYRSDEHRRPADIPDRFSAKBAHNAACVLTISPVPEDDADYICSVGVG 120

QY 121 FSP 123
 Db 121 FSP 123

RESULT 2
 US-09-425-335-2
 ; Sequence 2, Application US/09425335
 ; Patent No. 6518052
 ; GENERAL INFORMATION:
 ; APPLICANT: WEINMANN, ROBERTO
 ; TITLE OF INVENTION: HUMAN HOMOLOGUE OF YEAST HELICASE AND USES THEREOF
 ; FILE REFERENCE: db7 sequence
 ; CURRENT APPLICATION NUMBER: US/09/425.335
 ; CURRENT FILING DATE: 1999-10-22
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 689
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 US-09-425-335-2

Query Match 6.5%; Score 8; DB 4; Length 689;
 Best Local Similarity 100.0%; Pred.No. 6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108
 Db 149 TISPVQPE 156

RESULT 3
 US-08-162-102C-43
 ; Sequence 43, Application US/08162102C
 ; Patent No. 5762905
 ; GENERAL INFORMATION:
 ; APPLICANT: Burton, Dennis R.
 ; APPLICANT: Barbas, III, Carlos F.
 ; APPLICANT: Chanock, Robert M.
 ; APPLICANT: Murphy, Brian R.
 ; APPLICANT: Crowe, Jr., James E.
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/162,102C
 ; FILING DATE: 10-DEC-1993
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halle, Ph.D., Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07300/007001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 678-5070
 ; TELEFAX: (619) 678-5099
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 52 amino acids
 ; TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
JS-08-162-102C-43

Query Match 5.7%; Score 7; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88
|||||
DB 1 DIPDRFS 7

RESULT 4

JS-08-273-146-71
Sequence 71, Application US/08273146
Patent No. 5855885

GENERAL INFORMATION:

APPLICANT: Smith, Rodger
APPLICANT: McGafferty, John
APPLICANT: Chiswell, David
APPLICANT: Darsley, Michael J.
APPLICANT: Fitzgerald, Kevin
APPLICANT: Kenten, John H.
APPLICANT: Martin, Mark T.
APPLICANT: Titmas, Richard C.
APPLICANT: Williams, Richard O.
TITLE OF INVENTION: The Isolation and Production of
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273.146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-273-146-71.

Query Match 5.7%; Score 7; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89
|||||
DB 51 IPDRFSA 57

RESULT 5

US-08-276-852-92

Sequence 92, Application US/08276852

Patent No. 5652138

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-92

Query Match 5.7%; Score 7; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88
|||||
DB 53 DIPDRFS 59

RESULT 6

US-08-899-575-92

Sequence 92, Application US/08899575

Patent No. 5770440

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

RESULT 5

US-08-276-852-92

CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/899,575
 FILING DATE: 24-JUL-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 APPLICATION NUMBER: US 08/178,302
 FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/954,148
 FILING DATE: 30-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: SCR1452P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 S-08-899-575-92

Query Match 5.7%; Score 7; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 82 DIPDRFS 88
 |||||
 b 53 DIPDRFS 59

RESULT 7
 S-08-899-575-92
 Sequence 92, Application US/08899575
 Patent No. 580440
 GENERAL INFORMATION:
 APPLICANT: Burton, Dennis R
 APPLICANT: Barbas, Carlos F
 APPLICANT: Lerner, Richard A
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 170
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Scripps Research Institute, Office of
 ADDRESSEE: Patent Counsel
 STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
 STREET: Mail Drop 1PC8
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/899,575
 FILING DATE: 24-JUL-1997

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 APPLICATION NUMBER: US 08/178,302
 FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/954,148
 FILING DATE: 30-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: SCR1452P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-899-575-92

Query Match 5.7%; Score 7; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88
 |||||
 Db 53 DIPDRFS 59

RESULT 8
 PCT-US95-08743-92
 Sequence 92, Application PC/TUS9508743
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/08743
 FILING DATE: 11-JUL-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-08743-92

Query Match 5.7%; Score 7; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88
 |||||
 Db 53 DIPDRFS 59

RESULT 9
 US-08-162-102C-23
 Sequence 23, Application US/08162102C
 Patent No. 5762905

RESULT 13
US-09-425-638A-39
; Sequence 39, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader,
; APPLICANT: Lloyd J. Old

```

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 39
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
S-09-425-638A-39
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
|||||
RESULT 14
US-09-425-638A-40
Sequence 40, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 40
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-40
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
|||||
RESULT 15
US-09-425-638A-41
Sequence 41, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 41
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-41
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
|||||
RESULT 16
US-09-425-638A-42
Sequence 42, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 42
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-42
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
|||||
RESULT 17
US-09-425-638A-43
Sequence 43, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 43
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-43
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
|||||
RESULT 18
US-09-425-638A-44
Sequence 44, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 44

```

Y 53 GVSQYQQ 59

```
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
S-09-425-638A-44
    Query Match          5.7%; Score 7; DB 4; Length 109;
    Best Local Similarity 100.0%; Pred. No. 12;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Y 53 GVSWMYQQ 59
    b 32 GVSWMYQQ 38
    |||||
    |||||

RESULT 19
US-09-425-638A-45
; Sequence 45, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 45
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-45
    Query Match          5.7%; Score 7; DB 4; Length 109;
    Best Local Similarity 100.0%; Pred. No. 12;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Y 53 GVSWMYQQ 59
    b 32 GVSWMYQQ 38
    |||||
    |||||

RESULT 20
US-09-543-004-20
; Sequence 20, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 20
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-20
    Query Match          5.7%; Score 7; DB 4; Length 109;
    Best Local Similarity 100.0%; Pred. No. 12;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Y 53 GVSWMYQQ 59
    b 32 GVSWMYQQ 38
    |||||
    |||||

RESULT 21
US-09-543-004-21
; Sequence 21, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 21
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-21
    Query Match          5.7%; Score 7; DB 4; Length 109;
    Best Local Similarity 100.0%; Pred. No. 12;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Y 53 GVSWMYQQ 59
    b 32 GVSWMYQQ 38
    |||||
    |||||

RESULT 22
US-09-543-004-22
; Sequence 22, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 22
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-22
    Query Match          5.7%; Score 7; DB 4; Length 109;
    Best Local Similarity 100.0%; Pred. No. 12;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Y 53 GVSWMYQQ 59
    b 32 GVSWMYQQ 38
    |||||
    |||||

RESULT 23
US-09-543-004-39
; Sequence 39, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 23
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-20
    Query Match          5.7%; Score 7; DB 4; Length 109;
    Best Local Similarity 100.0%; Pred. No. 12;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Y 53 GVSWMYQQ 59
    b 32 GVSWMYQQ 38
    |||||
    |||||
```

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 39

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-39

Query Match 5.7%; Score 7; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSQYQQ 59

|||||

b 32 GVSQYQQ 38

RESULT 24

S-09-543-004-40

Sequence 40, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 40

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-40

Query Match 5.7%; Score 7; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSQYQQ 59

|||||

b 32 GVSQYQQ 38

RESULT 25

S-09-543-004-41

Sequence 41, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 41

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-41

Query Match 5.7%; Score 7; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSQYQQ 59

|||||

b 32 GVSQYQQ 38

RESULT 26

US-09-543-004-42

Sequence 42, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 42

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-42

Query Match 5.7%; Score 7; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSQYQQ 59

|||||

b 32 GVSQYQQ 38

RESULT 27

US-09-543-004-43

Sequence 43, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 43

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-43

Query Match 5.7%; Score 7; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSQYQQ 59

|||||

b 32 GVSQYQQ 38

RESULT 28

US-09-543-004-44

Sequence 44, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 44

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-44

Query Match 5.7%; Score 7; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSQYQQ 59

|||||

b 32 GVSQYQQ 38

RESULT 29

US-09-543-004-45

Sequence 45, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 45

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-45

Query Match 5.7%; Score 7; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSQYQQ 59

|||||

b 32 GVSQYQQ 38

CURRENT APPLICATION NUMBER: US/09/543,004
CURRENT FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 09/425,638
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129

SEQ ID NO 44

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-09-543-004-44

Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 53 GVSQYQQ 59

|||||

2b 32 GVSQYQQ 38

RESULT 29

US-09-543-004-45

Sequence 45, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 45

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-09-543-004-45

Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 53 GVSQYQQ 59

|||||

2b 32 GVSQYQQ 38

RESULT 30

PCT-US93-08786-23

Sequence 23, Application PC/TUS9308786

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R.

APPLICANT: Barbas, III, Carlos F.

APPLICANT: Chanock, Robert M.

APPLICANT: Murphy, Brian R.

APPLICANT: Crowe, Jr., James E.

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Spensley Horn Juba & Lubitz

STREET: 1880 Century Park East, Suite 500

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08786

FILING DATE: 16-SEP-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr., Ph.D., John R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: FD-2791

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: rsv 6L; 11L; 21L; anad 22L

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..109

PCT-US93-08786-23

Query Match 5.7%; Score 7; DB 5; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88

|||||

Db 58 DIPDRFS 64

RESULT 31

US-08-276-852-149

Sequence 149, Application US/08276852

Patent No. 5652138

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R.

APPLICANT: Barbas, Carlos F.

APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10686 No. 5652138th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276,852

FILING DATE: 18-JUL-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,302

FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
S-08-276-852-149

Query Match 5.7%; Score 7; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 82 DIPDRFS 88
b 58 DIPDRFS 64

RESULT 32
S-08-899-575-149
Sequence 149, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESSES:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
S-08-899-575-149

IS-08-899-575-149

Query Match 5.7%; Score 7; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88
DB 58 DIPDRFS 64

RESULT 33
US-08-899-575-149
Sequence 149, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESSES:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-149

Query Match 5.7%; Score 7; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88
DB 58 DIPDRFS 64

RESULT 34
PCT-US95-08743-149

Sequence 149, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-149

Query Match 5.7%; Score 7; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 IDPRFS 88
DB 58 IDPRFS 64

RESULT 35
US-08-480-753-6
; Sequence 6, Application US/08480753
; Patent No. 5830675
; GENERAL INFORMATION:
; APPLICANT: Targan M.D., Stephan R.
; APPLICANT: Vidulich Ph.D., Alda M.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
; TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF
; TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS, OR
; TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wendy A. Whiteford, Esq.
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,753
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whiteford, Wendy A.
; REGISTRATION NUMBER: 36,964
; REFERENCE/DOCKET NUMBER: P07 33571
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-480-753-6
Query Match 5.7%; Score 7; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 IDPRFS 89
DB 58 IDPRFS 64

RESULT 36
US-09-041-889-11
; Sequence 11, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-041-889-11

Query Match 5.7%; Score 7; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IDPRFS 89
DB 58 IDPRFS 64

RESULT 37
US-08-837-058-11
; Sequence 11, Application US/08837058
; Patent No. 6074835
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan

APPLICANT: Targan, Stephan R.
APPLICANT: Eggena, Mark
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Histone H1
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-837-058-11

Query Match 5.7%; Score 7; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89
| | | | |
Db 58 IPDRFSA 64

RESULT 38
US-09-417-264-11
; Sequence 11, Application US/09417264
; Patent No. 6537768
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Ofer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC panCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,889
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-417-264-11

Query Match 5.7%; Score 7; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89
| | | | |
Db 58 IPDRFSA 64

RESULT 39
US-09-328-352-6418
; Sequence 6418, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gazy L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6418
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6418

Query Match 5.7%; Score 7; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQLDA 27
| | | | |
Db 249 VLAQLDA 255

RESULT 40
US-09-266-965-140
; Sequence 140, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mac, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963

```
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 140
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Streptomyces lavendulae
US-09-266-965-140

Query Match      5.7%; Score 7; DB 4; Length 270;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 AQLDALL 29
DB      168 AQLDALL 174

RESULT 41
US-09-252-991A-21249
; Sequence 21249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21249
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21249

Query Match      5.7%; Score 7; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 LAQLDAL 28
DB      44 LAQLDAL 50

RESULT 42
US-08-457-176-2
; Sequence 2, Application US/08457176
; Patent No. 5591826
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5591826-Polypsis Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,175
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/457,176
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-457-176-2

Query Match      5.7%; Score 7; DB 1; Length 934;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 VLAQLDA 27
DB      598 VLAQLDA 604

RESULT 43
US-08-457-175-2
; Sequence 2, Application US/08457175
; Patent No. 5693470
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5693470-Polypsis Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,175
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; CURRENT APPLICATION DATA:
```

TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 934 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-457-175-2

Query Match 5.7%; Score 7; DB 1; Length 934;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 21 VLAQLDA 27
b 598 VLAQLDA 604

RESULT 44

US-08-709-784-1
Sequence 1, Application US/08709784
Patent No. 6048701
GENERAL INFORMATION:

APPLICANT: The Johns Hopkins University
TITLE OF INVENTION: Antibody Detection of Mismatch Repair
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,784

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/480,351

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 1107.57434

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 934 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-709-784-1

Query Match 5.7%; Score 7; DB 3; Length 934;
Best Local Similarity 100.0%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 VLAQLDA 27
Db 598 VLAQLDA 604

RESULT 45

US-09-651-656-3
Sequence 3, Application US/09651656
Patent No. 6340566
GENERAL INFORMATION:

APPLICANT: MCCUTHEN-MALONEY, SANDRA

APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY

TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE

TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,

TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES

FILE REFERENCE: IL-10689

CURRENT APPLICATION NUMBER: US/09/651,656

CURRENT FILING DATE: 2000-08-29

PRIOR APPLICATION NUMBER: 60/192,764

PRIOR FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 3

LENGTH: 934

TYPE: PRT

ORGANISM: Homo sapiens

US-09-651-656-3

Query Match 5.7%; Score 7; DB 4; Length 934;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQLDA 27
Db 598 VLAQLDA 604

RESULT 46

US-09-650-855-3

Sequence 3, Application US/09650855

Patent No. 6365355

GENERAL INFORMATION:

APPLICANT: MCCUTHEN-MALONEY, SANDRA

APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY

TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA

TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA

TITLE OF INVENTION: MISMATCHES

FILE REFERENCE: IL-10284

CURRENT APPLICATION NUMBER: US/09/650,855

CURRENT FILING DATE: 2000-08-29

PRIOR APPLICATION NUMBER: 60/192,764

PRIOR FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 3

LENGTH: 934

TYPE: PRT

ORGANISM: Homo sapiens

US-09-650-855-3

Query Match 5.7%; Score 7; DB 4; Length 934;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQLDA 27
Db 598 VLAQLDA 604

RESULT 47

US-09-708-200-13

; Sequence 13, Application US/09708200
; Patent No. 6576468
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sasse, Philip M
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
; FILE REFERENCE: HYPERMUTABLE CELLS
; CURRENT APPLICATION NUMBER: US/09/708,200
; CURRENT FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-708-200-13

Query Match 5.7%; Score 7; DB 4; Length 934;
Best Local Similarity 100.0%; Pred. No. 79; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 21 VLAQLDA 27
| | | | |
Db 598 VLAQLDA 604

RESULT 48
US-09-512-250C-31
; Sequence 31, Application US/09512250C
; Patent No. 6518042
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis
; APPLICANT: Wind, Jesper
; TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells
; FILE REFERENCE: No. 6518042el Cloned Gene Involved in the Mismatched Repair Syst
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 5718.200-US
; CURRENT APPLICATION NUMBER: US/09/512,250C
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 31
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: human.p
US-09-512-250C-31

Query Match 5.7%; Score 7; DB 4; Length 1010;
Best Local Similarity 100.0%; Pred. No. 85; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 21 VLAQLDA 27
| | | | |
Db 674 VLAQLDA 680

RESULT 49
US-09-252-991A-28966
; Sequence 28966, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

Query Match 4.9%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 66 RYLLY 71
| | | | |
Db 2 RYLLY 7

RESULT 51
US-08-476-405A-1
; Sequence 1, Application US/08476405A
; Patent No. 5776459
; GENERAL INFORMATION:
; APPLICANT: Vandenberg, Arthur A.

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28966
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28966

Query Match 5.7%; Score 7; DB 4; Length 1039;
Best Local Similarity 100.0%; Pred. No. 87; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 74 EEDHRP 80
| | | | |
Db 976 EEDHRP 982

RESULT 50
US-08-747-599A-17
; Sequence 17, Application US/08747599A
; Patent No. 6214795
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Howard et al.
; TITLE OF INVENTION: Peptide Compounds Useful for Modulating
; TITLE OF INVENTION: FGF Receptor Activity
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/747,599A
; APPLICATION NUMBER: 12-NOV-1996
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-747-599A-17

Query Match 4.9%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 66 RYLLY 71
| | | | |
Db 2 RYLLY 7

RESULT 51
US-08-476-405A-1
; Sequence 1, Application US/08476405A
; Patent No. 5776459
; GENERAL INFORMATION:
; APPLICANT: Vandenberg, Arthur A.

;; TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides

;; NUMBER OF SEQUENCES: 27

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Connective Therapeutics, Inc.

;; STREET: 3400 West Bayshore Road

;; CITY: Palo Alto

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94303

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/476,405A

;; FILING DATE:

;; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/059,020

;; FILING DATE: 16-MAR-1993

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/735,612

;; FILING DATE: 16-JUL-1991

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/708,022

;; FILING DATE: 31-MAY-1991

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/554,529

;; FILING DATE: 19-JUL-1990

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/467,577

;; FILING DATE: 19-JAN-1990

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/382,804

;; FILING DATE: 19-JUL-1989

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Lowin, David A.

;; REGISTRATION NUMBER: 29,326

;; REFERENCE/DOCKET NUMBER: 886 P15

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 415-843-2800

;; TELEFAX: 415-843-2899

;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; JS-08-476-405A-1

Query Match 4.9%; Score 6; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; 54 VSWYQQ 59

;; |||||

;; 8 VSWYQQ 13

RESULT 52

JS-08-658-136-23

;; Sequence 23, Application US/08658136

;; Patent No. 6071717

;; GENERAL INFORMATION:

;; APPLICANT: KLINGER, KATHERINE W

;; APPLICANT: LANDES, GREGORY M

;; APPLICANT: BURN, TIMOTHY C

;; APPLICANT: CONNORS, TIMOTHY D

;; APPLICANT: DACKOWSKI, WILLIAM

;; APPLICANT: GERMINO, GREGORY

;; APPLICANT: QIAN, FENG

;; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE

;; NUMBER OF SEQUENCES: 58

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: GENZYME CORPORATION

;; STREET: ONE MOUNTAIN ROAD

;; CITY: FRAMINGHAM

;; STATE: MASSACHUSETTS

;; COUNTRY: USA

;; ZIP: 01701

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/658,136

;; FILING DATE:

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: LASSEN, ELIZABETH

;; REGISTRATION NUMBER: 31,845

;; REFERENCE/DOCKET NUMBER: GEN4-17.8

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 508-872-8400

;; TELEFAX: 508-872-5415

;; INFORMATION FOR SEQ ID NO: 23:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 20 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-658-136-23

Query Match 4.9%; Score 6; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 QVAQLS 39

Db 10 QVAQLS 15

RESULT 53

US-09-690-454-102

;; Sequence 102, Application US/09690454

;; Patent No. 6531447

;; GENERAL INFORMATION:

;; APPLICANT: Steven M. Ruben, et al.

;; TITLE OF INVENTION: 32 Human Secreted Proteins

;; FILE REFERENCE: P2006P1

;; CURRENT APPLICATION NUMBER: US/09/690,454

;; CURRENT FILING DATE: 2000-10-18

;; PRIOR APPLICATION NUMBER: 09/189,144

;; PRIOR FILING DATE: 1998-11-10

;; PRIOR APPLICATION NUMBER: 60/044,039

;; PRIOR FILING DATE: May 30, 1997

;; PRIOR APPLICATION NUMBER: 60/048,093

;; PRIOR FILING DATE: May 30, 1997

;; PRIOR APPLICATION NUMBER: 60/048,190

;; PRIOR FILING DATE: May 30, 1997

;; PRIOR APPLICATION NUMBER: 60/050,935

;; PRIOR FILING DATE: May 30, 1997

;; PRIOR APPLICATION NUMBER: 60/048,101

;; PRIOR FILING DATE: May 30, 1997

;; PRIOR APPLICATION NUMBER: 60/048,356

;; PRIOR FILING DATE: May 30, 1997

;; PRIOR APPLICATION NUMBER: 60/056,250

;; PRIOR FILING DATE: August 29, 1997

;; PRIOR APPLICATION NUMBER: 60/056,296

;; PRIOR FILING DATE: August 29, 1997

;; PRIOR APPLICATION NUMBER: 60/056,293

;; PRIOR FILING DATE: August 29, 1997

;; NUMBER OF SEQ ID NOS: 229

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-690-454-102
Query Match 4.9%; Score 6; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DALLVF 31
Db 8 DALLVF 13

RESULT 54
US-08-162-102C-44
; Sequence 44, Application US/08162102C
; Patent No. 5762905
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R.
; APPLICANT: Barbas, III, Carlos F.
; APPLICANT: Chanock, Robert M.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Crowe, Jr., James E.
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,102C
; FILING DATE: 10-DEC-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07300/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-162-102C-44
Query Match 4.9%; Score 6; DB 1; Length 53;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 2 IPDRFS 7

RESULT 55
US-08-851-843A-183
; Sequence 183, Application US/08851843A
```

```
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-843A-183
Query Match 4.9%; Score 6; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LSCITLS 43
Db 46 LSCITLS 51

RESULT 56
US-08-974-549A-302
; Sequence 302, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
```

APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 302:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-302

Query Match 4.9%; Score 6; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

38 LSCTLS 43
|||||

Db 46 LSCTLS 51
RESULT 57
US-08-854-050-183
; Sequence 183, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-854-050-183

Query Match 4.9%; Score 6; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 38 LSCTLS 43
|||||
Db 46 LSCTLS 51

RESULT 58

US-09-430-323-183
; Sequence 183, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Morin, Gregg B.
; Chapman, Karen B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-09-430-323-183

Query Match 4.9%; Score 6; DB 4; Length 54;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LSCTLS 43

Db 46 LSCTLS 51

RESULT 59

US-08-765-179B-19
; Sequence 19, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:

; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,179B
; FILING DATE: 14-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BP95/02626
; FILING DATE: 06-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 25 115.7
; FILING DATE: 15-JUL-1994
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-765-179B-19
Query Match 4.9%; Score 6; DB 2; Length 64;
Best Local Similarity 100.0%; Pred.No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 VSWYQQ 59
Db 2 VSWYQQ 7
RESULT 60
US-08-273-146-67
; Sequence 67, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phase Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/273,146

FILING DATE: 14-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ryan, John W.

REGISTRATION NUMBER: 33,771

REFERENCE/DOCKET NUMBER: 09000

TELEPHONE: 301-984-8000

TELEFAX: 301-230-0158

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 67 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

IS-08-273-146-67

Query Match 4.9%; Score 6; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 83 IPDRFS 88

b 14 IPDRFS 19

RESULT 61

IS-09-003-198A-17

Sequence 17, Application US/09003198A

Patent No. 6316407

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip Maganlal

APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,198A

FILING DATE: 07-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 72 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

IS-09-003-198A-17

IS-09-003-198A-17

Query Match 4.9%; Score 6; DB 4; Length 72;

Best Local Similarity 100.0%; Pred. No. 82;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLL 10

Db 8 CLSFLL 13

RESULT 62

US-08-476-405A-25

Sequence 25, Application US/08476405A

Patent No. 5776459

GENERAL INFORMATION:

APPLICANT: Vandenberg, Arthur A.

TITLE OF INVENTION: Method of Treatment Using TCR Vbetas Peptides

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Connective Therapeutics, Inc.

STREET: 3400 West Bayshore Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,405A

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/059,020

FILING DATE: 16-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,612

FILING DATE: 16-JUL-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/708,022

FILING DATE: 31-MAY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/554,529

FILING DATE: 19-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/467,577

FILING DATE: 19-JAN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/382,804

FILING DATE: 19-JUL-1989

ATTORNEY/AGENT INFORMATION:

NAME: Lowin, David A.

REGISTRATION NUMBER: 29,326

REFERENCE/DOCKET NUMBER: 886 P15

TELEPHONE: 415-843-2800

TELEFAX: 415-843-2899

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 82 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-476-405A-25

Query Match 4.9%; Score 6; DB 1; Length 82;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59

Db 20 VSWYQQ 25

RESULT 63

US-08-181-492B-27

; Sequence 27, Application US/08181492B

; Patent No. 5552300

; GENERAL INFORMATION:

; APPLICANT: Makrides, Savvas C

; APPLICANT: Kung, Patrick C

; TITLE OF INVENTION: T Cell Antigen Receptor V Region

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: T Cell Sciences, Inc.

; STREET: 115 Fourth Avenue

; CITY: Needham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 02194-2725

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: MS-DOS 6.2

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/181,492B

; FILING DATE: 13-January-1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Yankwich, Leon R.

; REGISTRATION NUMBER: 30,237

; REFERENCE/DOCKET NUMBER: TCS-203-P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-345-9110

; TELEFAX: 617-345-9111

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 92 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL:

; ANTI-SENSE:

; FEATURE:

; NAME/KEY:

; LOCATION:

; US-08-181-492B-27

Query Match

Best Local Similarity 4.9%; Score 6; DB 1; Length 92;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59

DB 30 VSWYQQ 35

RESULT 64

PCT-US95-00408-27

; Sequence 27, Application PC/TUS9500408

; GENERAL INFORMATION:

; APPLICANT: T Cell Sciences, Inc

; TITLE OF INVENTION: T Cell Antigen Receptor V Region Proteins

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: T Cell Sciences, Inc.

; STREET: 1515 Fourth Avenue

; CITY: Needham

Query Match 4.9%; Score 6; DB 4; Length 94;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 02194-2725

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/00408

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,492

; FILING DATE: 13-January-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: YANKWICH, Leon R.

; REGISTRATION NUMBER: 30,237

; REFERENCE/DOCKET NUMBER: TCS-203-PCT(94,664-A)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-345-9100

; TELEFAX: 617-345-9111

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 92 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL:

; ANTI-SENSE:

; FEATURE:

; NAME/KEY:

; LOCATION:

; PCT-US95-00408-27

Query Match

Best Local Similarity 4.9%; Score 6; DB 5; Length 92;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59

DB 30 VSWYQQ 35

RESULT 65

US-09-732-210-818

; Sequence 818, Application US/09732210

; Patent No. 6573361

; GENERAL INFORMATION:

; APPLICANT: Bunkers, Greg J.

; APPLICANT: Liang, Jihong

; APPLICANT: Mittanck, Cindy A.

; APPLICANT: Seale, Jeffrey W.

; APPLICANT: Wu, Yonnie S.

; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use

; FILE REFERENCE: 38-21(15036)B

; CURRENT APPLICATION NUMBER: US/09/732,210

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,513

; PRIOR FILING DATE: 1999-12-07

; PRIOR APPLICATION NUMBER: US 60/169,340

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 1753

; SEQ ID NO 818

; LENGTH: 94

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

; US-09-732-210-818

Query Match 4.9%; Score 6; DB 4; Length 94;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 60 RAGSAP 65
|||||
b 72 RAGSAP 77

RESULT 66

S-08-488-113B-158
Sequence 158, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-158

Query Match 4.9%; Score 6; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 54 VSWYQQ 59
|||||
b 32 VSWYQQ 37

RESULT 68

US-08-107-669D-22
Sequence 22, Application US/08107669D
Patent No. 5766886
GENERAL INFORMATION:

RESULT 67

US-08-477-484B-158
Sequence 158, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-158

Query Match 4.9%; Score 6; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 VSWYQQ 59
|||||
Db 32 VSWYQQ 37

APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2540
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-669D-22

Query Match 4.9%; Score 6; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 VSWYQQ 59
Db 32 VSWYQQ 37

RESULT 69
US-08-472-788A-22
Sequence 22, Application US/08472788A
Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-22

Query Match 4.9%; Score 6; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 VSWYQQ 59
Db 32 VSWYQQ 37

RESULT 70
US-08-477-531B-22
Sequence 22, Application US/08477531B
Patent No. 5821123
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-531B-22

Query Match 4.9%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 54 VSWYQQ 59
Db 32 VSWYQQ 37

RESULT 71

US-08-646-360-158
Sequence 158, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-158

Query Match 4.9%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 54 VSWYQQ 59
Db 32 VSWYQQ 37

RESULT 72

US-08-082-842A-22
Sequence 22, Application US/08082842A
Patent No. 5869619
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-JUN-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-22

Query Match 4.9%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 54 VSWYQQ 59
Db 32 VSWYQQ 37

RESULT 73

US-08-839-765-158
Sequence 158, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-158

Query Match 4.9%; Score 6; DB 3; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59
DB 32 VSWYQQ 37

RESULT 74
US-09-136-389-158
Sequence 158, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-158

Query Match 4.9%; Score 6; DB 3; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59
DB 32 VSWYQQ 37

RESULT 75
US-09-610-838-158
Sequence 158, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
S-09-610-838-158

Query Match 4.9%; Score 6; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 54 VSWYQQ 59
b 32 VSWYQQ 37

Search completed: February 9, 2004, 13:04:19
Job time: 23 secs